

FIGURE 1

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATCCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCACAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCTTGGGC
TCCAGCAGCATCAGCAGCCCCAGGACCGGGGGAGGCACAGGTGGCCCCCACCACCCGGAGG
AGCAGCTCCTGCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGA
AGGCCACCCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT
TCTGTTGTTGGCAGTGGGCGGCACAGAGCACGCCCTACCGGCCCGGCCGTTAGGGTGTGTGCT
GTCCCGGGCTCACGGGGACCTGTCTCCGAGTCGTTCTGTGACGCGTGTGTACCAGCCCTTCC
TCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATTTATAGGACCGCCTAC
CGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAG
GACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCATGCCGGAACGGAG
GGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG
TCAGATGTGGATGAATGCAGTGTCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGC
CGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG
TGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAG
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCT
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC
TCCTGGTGCACCTCTCCAGCAGCTCGGCCGATCGACTCCCTGAGCGAGCAGATTTCCTTC
CTGGAGGAGCAGCTGGGGTCTGTCTCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGG
CTGGACTGAGCCCCCTACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTC
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCCTTTTCTCCTC
CCCTTCCCTCGGGAGGGTCCCCAGACCCTGGCATGGGATGGGTGGGATTTTTTTGTGAAT
CCACCCCTGGCTACCCCAACCCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA
GCTGAGGGAAGGTACGAGTTCCCTGCTGGAGCCTGGGACCATGGCACAGGCCAGGCAGCC
CGGAGGCTGGGTGGGGCTCAGTGGGGCTGCTGCCTGACCCCCAGCACAATAAAAAATGAAA
CGTGAAAAA
AGAGTCGACCTGCAGAAGCTTGGCCGCATGGCCCACTTGTTATTGCAGCTTATAATGGT
TACAAAT

FIGURE 2

MTDSPPPGHPPEEKATPPGGTGHEGLSGGAADVASGVSGRHRARLPARPLGCVLSTRAHGDPV
SESFVQVRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC
GAAICQPPCRNGGSCVQPGRCRCPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCW
EGHSLSADGTLCPVKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLAS
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 93-97, 270-274

N-myristoylation sites.

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,
191-197, 265-271

Amidation site.

amino acids 26-30

Aspartic acid and asparagine hydroxylation site.

amino acids 152-164

Cell attachment sequence.

amino acids 130-133

EGF-like domain cysteine pattern signature.

amino acids 123-135

FIGURE 3

CGCTCGCCCCGTGCGCCCTCGCCTCCCCGAGAGTCCCTCGCGGCAGCAGATGTGTGTGGG
 GTCAGCCACGGCGGGGACTATGTGAAATTCCTCGGCGCTCACGCACTACTGCCCCCTGATC
 CGGTTCTTGGTGCCCCCTGGGCATCACCAACATAGCCATCGACTTCGGGGAGCAGGCCTTGAA
 CCGGGGCATTGCTGCTGTCAAGGAGGATGCACTCGAGATGCTGGCCAGCTACGGGCTGGCGT
 ACTCCCTCATGAAGTCTTCCACGGGTCCCATGAGTGACTTCAAAAATGTGGGCTGGTGT
 GTGAACAGCAAGAGAGACAGGACCAAGGCCCTCTGTGTATGGTGTGGCAGGGGCCATCGC
 TGCCGCTCTTTACACACTGATAGCTTATAGTGATTTAGGATACTACATTATCAATAAACTGC
 ACCATGTGGACGAGTGGTGGGGAGCAAGACGAGAAGGCCCTCTCTGATCTCGCCGCTTT
 CCTTTCATGGACGAATGGCATGGACCCATGCTGGCATTCTCTTAAAAACAAATACAGTTT
 CCTGGTGGGATGTGCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTGTAGCCATTTTGC
 TTCACAGTCACTGGAAATGCCGGGAGCCCCGTGCTCATCCCGATCTCTCCTTGTACATGGGC
 GCACTTGTGCGCTGCACCACCTGTGCTGGGCTACTACAAGAACATTACAGCATCATCCC
 TGACAGAAGTGGCCCCGAGCTGGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT
 GGCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCTATTGTCAACCTCTTGT
 TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGCAGTGGCGATTTTGACAGCCACATA
 CCTCTGGGTACATGCCATCGGCTGGTTGACGGAAATCCGTGTGTATCTCGTCTTTCG
 ACAAGAATAACCCAGCAACAAACTGGTGAGCACGAGCAACACAGTCACGGCAGCCACATC
 AAGAAGTTCACCTTCTGCTGTCATGGCTCTGTCACTCAGCTCTGTCTTGTGATGTTTGGAC
 ACCAACGCTGTGAGAAAATCTTGATAGACATCATCGGATGGACTTTGCTCTTTGCAGAAC
 TCTGTGTTGTTCTTTGGCGATCTTCTCCTTCTTCCAGTTCAGTCACAGTGAGGGCGCAT
 CTCACCGGCTGGCTGATGACACTGAAGAAAACCTTCGTCTTGGCCCCAGCTCTGTGCTCG
 GATCATCGTCTCATCGCCAGCTCGTGGTCTTACCTACTGGGGGTGCACGGTGCAGACC
 TGGGCGTGGGCTCCCTCCTGGCGGCTTGTGGGAGAATCCACCATGGTCGCCATCGCTCGG
 TGCTATGCTACCGGAAGCAGAAAAGAAGATGGAGAATGAGTCGGCCACGGAGGGGAAGA
 CTCTGCCATGACAGACATGCTCCGACAGAGGAGGTGACAGACATCGTGGAAATGAGAGAG
 AGAATGAATTAAGGCACGGGACGCCATGGGCATGACGGGACGGTCAGTCAGGATGACATTC
 GGCACTCATCTCTCCCTCTCCCATCGTATTTTGTTCCTTTTGTGTTTTGTTTTGGTAAT
 GAAAGAGGCTTGTATTAAGGTTTCGTGTCAATTCTCTAGCATACTGGGTATGCTCACACT
 GACGGGGGACCTGAGTTAATGGTCTTTACTGTTGCTATGTAAAAACAAACGAAACAACCTGAC
 TTCATACCCCTGCCTCACGAAAACCCAAAAGACACAGCTGCCTCACGGTTGACGTTGTGTCC
 TCCTCCCCCTGGACAATCTCCTCTTGAACCAAAGGACTGCAGCTGTGCCATCGCGCTCGGT
 CACCTGTGCACAGAGCCACAGACTCTCCTGTCCCTTCATCGTCTTAAGAATCAACAGG
 TTAAAACTCGGCTTCCTTTGATTTGCTTCCAGTCAATGGCCGTACAAGAGATGGAGCCC
 CGGTGGCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACACATGCAG
 GAGGCGGGTGGCACGCTGTCAGCCCGAGTCCCCGTTACACTGAGGAACGGAGACCTGTGAC
 CACAGCAGCTGACAGATGGACAGAAATCTCCCGTAGAAAGGTTTGGTTTGAATGCCCCGGG
 GGCAGCAACTGACATGGTTGAATGATAGCATTTCACTCTCGCTTCTCTAGATCTGAGCAA
 GCTGTGAGTTCTCACCCCCACCGTGTATATACATGAGCTAACTTTTTTAAATTTGTCACAAA
 GCGCATCTCCAGATTCAGACCCCTGCCGATGACTTTTCTGGAAGGCTTGCTTTTCCCTCGC
 CTTTCTGGAAGGTGCGATTAGAGCGAGTACATGGAGCATCTCACTTGTGATTTGATTTT
 TACAGTGAACCTGAAGCTTTAAGTCTCATCCAGCATTTCTAATGCCAGGTTGCTGTAGGGTAA
 CTTTTGAAGTAGATATATTACCTGGTCTGCTATCTTAGTCATAACTCTGCGGTACAGGTAA
 TTGAGAATGTACTACGGTACTTCCCTCCACACCATCATGATAAGCAAGACATTTATAACG
 ATACAGAGTCACTATGTGGTCTCCCTGAAATAACGCATTCGAATCCATCGAGTGAGTGA
 TATTTTCTAAGTTTGGGAAAGCAGGTTTTTCCCTTAAAAAAATATAGACACGGTTCAGT
 AAATTGATTTAGTCAGAATTCCTAGACTGAAAGAACCTAAACAAAAAAATATTTTAAAGATA
 TAAATATATGCTGTATATGTTATGTAATTTATTTAGGCTATAATACATTTTCTATTTTCG
 ATTTTCAATAAATGCTCTAATACAAAAA

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FIGURE 4

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF
TGPMSEDFKNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSIDLGYIIINKLHHVDESV
GSKTRRAFLYLAAFPFMDAMANTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC
REPLLIPIILSLYMGALVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL
ATQIRISRPVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN
KLVSTSNVTAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFaelcVvPLR
IFSFFPVVPTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYLGvHGATLGvGSLl
AGFVGESTMVAIAACVYVRKQKKKMenESATEGEDSAmTDMpPTEEVTDIVEMREENE

Transmembrane domains:

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,
408-423, 431-445

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FIGURE 5

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTTCG
ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCGGCCACATC
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTGGAC
ACCCAACGTGTCTGNAAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC
TCTGTGTTGTTCTTTGCGGATCTTCTCCTTCTTCCCAGTTCCAGTCACAGTGAGGGCGCAT
CTCACCGGTGGCTGATGACACTGAAGAAAACCTTCGTC

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FIGURE 6

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAAACCCCAAGCAANAAATTGGG
GAGCAGGGCAAAACAGTNACGGGCAGCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAATTTTGAT
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTCCCTTTGCGGATTTTCT
CCTTTTCCAGTTCCAGTCACAGNGAGGGCGCATCTACCGGGNGGNTGATGACANTGAAG
AAAACCTTTGTCCTTGCCCCAGCTNTTTGGTGCGGATCATTTGCCTNATNGCCAGCCTTGT
GGTCCTACCCTACCTGGGGGTGCACGGTGCGACCTGGGCGTGGGTTCCCTCCTGGCGGGCA

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FIGURE 7

TATTCCCAGTTCCGGTCACGGGGAGGGCGCATNTCACCGGGTGGCTGANGACACTGAAGAAA
ACCTTNGTCCTTGCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT
CCTACCCTACCTGGGGGTGCACGGTGAGAC

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FIGURE 8

GCCTGCTCCCTGCTCAGCTGCGCGTCTGCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG
CTGCTGCCCCGCGCAGCCGCAACTCCACCGTGAGCCGCGCTCATCTTCACGTTCTTCTCTTCC
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTG
CCCTGGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCTGTCAGGGCCACATCGACTGTGG
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGCGCTTCTTCTTCT
TCTTTTTCACCCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG
AATGGGTTTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCTCACCGTGGGTGCCTTCTACAT
CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGCTGCTGGGCTCCTTCTCTTCA
TCCTCATCCAGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACAGCGGTGGCTGGGC
AAGGCCGAGGAGTGCGATTCCCGTGCTGGTACGCAAGGCTCTTCTTCTTCACTCTCCTCTT
CTACTTGCTGTGATCGCGGCGGTGGCGCTGATGTTTATGTTACTACTGAGCCCAAGCGGCT
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGCTGCGTGCATCGCT
GCTGTCTGCCCCAAGTCCAGGACGCCAGCCCAACTCGGGTCTGCTGCAGGCTCGGTGAT
CACCCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA
ACCCCATTTTGCCAACCCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG
ACCCAGTGGTGGGATGCCCCGAGCATGTGGGCTCATCATCTTCTCTCTGTGCACCCCTCTT
CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCAGGAGTGCC
CACCTATGTAGTAGCGCCACACAGCAGCAGCAGCAGAGGTGGCAGCCTGTGAGGGCCGGGCC
TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCTTCTTCCACTTCTGCTGGTGTCT
GGCCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA
TGATCAGCACGTGGACCGCGCTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC
TACCTGTGGACCTTGGTAGCCCCACTCTCTCTGCGCAACCGCGACTTCAGCTGAAGCAGCCT
CACAGCCTGCCATCTGGTGCTCTCTGCCACCTGGTGCTCTCGGCTCGGTGACAGCCAACCT
GCCCCCTCCCCACCAACTCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTG
CCCCTGAGCCGGGCTTCTAGTCTGATGCTTTCAGGCTCCGAGGAGCATCAGGCTCTCTGCA
GAGCCCCATCCCCCGCCACACCCACAGGTGGAGCTGCCTTCTTCTTCCCTCCTCCTCTGT
TGCCATACTCAGCATCTCGGATGAAAGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGG
CTGCTGGAGAGAGCGGGAACTCCACCACAGTGGGGCATCCGGCACTGAAGCCCTGGTGT
CCTGGTCAGTCCCCCAGGGGACCTGCCCTTCTCTGGACTTCGTGCCTTACTGAGTCTCT
AAGACTTTTCTAATAAACAGCCAGTGCGTGTAAAAAAA

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Signal sequence:

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 10

GAGCGAGGCCGGGGACTGAAGGTGTGGGTGTCTGAGCCCTCTGGCAGAGGGTTAACCTGGGTG
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCCGGGCACGTCCGCGAGGACTTGA
AGTCTCTGAGCGCTCAAGTTTGTCCGTAGGTGAGAGAGAGGCCATGGAGGTGCCGCCACCGGC
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCATTTCCTCCGAGTCTTTGCTGCCGAAGCTG
TGACTGCCGATTGGAAGTCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCGAGAGCCC
TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG
TGTATGGGGGAATACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACAGAGGCTT
CATTCGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTGTTGTGACTATATTCAACACAG
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAATTGCAGGA
GCTGTCACGGGAAGTCTTTTAGGATAAACGTAAGCCTGCGTGGCCTGGTGGCTGGTGGCAT
AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCAATTCAGAAGTACGCTG
GTGAGACTGTTTCAGGAAAGAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACTGGAA
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAAATTGAAAGTAGTTTACG
GGAAGATGAACCTGAGAATGATGCTAAGAAAAATTGAAGCACTGCTAAACCTTCCTAGAAAAC
CTTCAGTAATAGATAAAACAAGACAAGGACTTGAAAGTGCTCTGAACTTGAACTCACTGGAGA
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCACCTCTTTGGTCAGCCTGC
TGACAAATTTAAGTGCTGTACCTGTGGTGGCAGTGGCTTGCTCTTGTCTTTTTCTTTCTTT
TTTAACTAAGAATGGGGCTGTTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT
TATGTTTGTATTAACTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA
GCAGTAAATAAAACATTTTCGCAAAAGATTAAAGTTGAATTTTACAGTTT

FIGURE 11

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32190, pI: 9.03, NX(S/T): 2
MEVPPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAIEIYHNRFDVQSAH
RAATRGFIRYGWRWGWRTAVFVTIFNTVNTSLNVYRNKDLSHFVIAGAVTGSLSLFRINVGLR
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPE
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

Important Features:

Signal Peptide:

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

FIGURE 12

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTTGGCTGGGTGTATGGGGGAA
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT
AACC GGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTTCGTTTCATG
GCTGGCGCCGAACC

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FIGURE 13

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT
TTTTCTGTAGAGCATTGTGCCTATTTCCCGAGTTTTTGCTGCCGAAGCTGTGACTGCCGAT
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA
ATACCAGCTTTTATTTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA
TAACC

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FIGURE 14

GAGCCGCCGCCGCCGCCGCCGCCGCTGCAGCCCCAGGCCGCCGCCGCCACCCACGTCT
GCGTTGCTGCCCCGCCCTGGGCCAGGCCCAAAGGCAAGGACAAGCAGCTGTCAGGGAACCT
CCGCCGGAGTCGAATTTACGTGCAGCTGCCGCCAACCACAGGTTCCAAGATGCTTTGCGGGG
GCTTCGCGTGTTCGAAGAACTGCGCTGTGCGCCCTCAACCTGCTTTACACCTTGGTTAGTCTG
CTGCTAAATTGGAATTGCTGCGTGGGGCATTTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGT
CGGCGTGGTCATTCAGTGGGCATCTTCTTGTTCCTGATTGCTTTAGTGGGTCTGATTGGAG
CTGTAAAACATCATCAGGTGTTGCTATTTTTTTATATGATTATTCTGTTACTTGTATTTATT
GTTCAGTTTTTCTGTATCTTGCCTTGTTTAGCCCTGAACCAGGAGCAACAGGTCAGCTTCT
GGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCT
GTGGGTTTCGAAGTGTTAAACCAATGACACCTGTCTGGCTAGCTGTGTTAAAAGTGACCAC
TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTGTAGATTTGTTGG
TGGCATTGGCCTGTTCTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACCTACAGATAACA
GGAACCAGAAAGACCCCCGCCGCAATCCTAGTGCAATTCCTTTGATGAGAAAACAAGGAAT
TTCCTTTCGTATTATGATCTTGTTCACTTTCTGTAATTTTCTGTTAAGCTCCATTTGCCAGT
TTAAGGAAGGAAACACATATCTGAAAAGTACCTTATGATAGTGAATTATATATTTTTACT
CTATGTTTCTCTACATGTTTTTTTCTTTCCGTTGCTGAAAAATATTTGAAACTTGTGGTCTC
TGAAGCTCGGTGGCACCTGGAATTTACTGTATTTCATTGTCGGGCACTGTCCACTGTGGCCTT
TCTTAGCATTTTTTACCTGCAGAAAACTTTGTATGTTACCACTGTGTTGGTTATATGGTGAA
TCTGAACGTACATCTCACTGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCTTAC
TGGAAAAAGAGTGAAATTTATTAATCAGAAAGTATGAGATCCTGTTATGTTAAGGGAAA
TCCAAATCCCAATTTTTTTTGGTCTTTTATAGAAAGATTGTTGTGGTAAAAAGTGTAGTA
TAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAAATAGTTAT
GTCTTAGGAAATTGTGGTTTAATTTTTTGACTTTTACAGGTAAGTGCAAGGAGAAGTGGTTT
CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCTCCATCAGAATGGAACGAGTTT
TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTTATAATAATTTGAAGTCTAA
AAGACTGCATTTTAAACAAGTTAGTATTAATGCGTTGGCCCACGTAGCAAAAAGATATTTG
ATTATCTTAAAAATTGTTAAATACCGTTTTCATGAAATTTCTCAGTATTGTACAGCAACTT
GTCAAACTAAGCATATTTGAATATGATCTCCATAATTTGAAATGAAATCGTATTGTGTG
GCTCTGTATATTCTGTTAAAAAATTAAAGGACAGAAACCTTTCTTGTGTATGCATGTTTGA
ATTAAAGAAAGTAATGGAAG

FIGURE 15

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIAGVIGFLFLIALV
GLIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACLALNQEQQGQLLEVGNNTASARNDIQR
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRFBVGIGLFFSFTEILGVWL
TYRYRNQKDFRANPSAFL

Signal Peptide:

amino acids 1-34

Transmembrane domains:

amino acids 47-63, 72-95 and 162-182

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TOSTI-8812/60

FIGURE 16

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTTATATGATTATTCGTAAANT
TGTATTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT
NTAAACTGCTGTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTNTGGCTAGCTGTGTAA
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA
GATTTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC
TACAGATACAGGAACCAG

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FIGURE 17

AATCCCAAATCCCCAATTTTTTTGGNCITTTTAGGGAAAGATGTGTTGTGGTAAAAAGTGT
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG
TTATGTCTTAGGAAATTGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG
TCTAAAAGACTGCATTTTTAAACAAGTTAGTATTAAATGCGTTGGCCCACGTAGCAAAAAGAT
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAAACAGC
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATT
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC
CCACTTGC

INSTANT 2218/660

FIGURE 18

ATGATTATTCTGTTACTTGTATTTATTGTTTCAGTTTTATGGTATCTTGCGCTTGTTTAGCCC
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG
TGACTCCGCAAATGACATCCAGAGAAATCCTAAACTGCTGTGGGTTCCGAAGTGTTAACCC
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA
TCATAGGAGAATATGC

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FIGURE 19

CAGTCACCATGAAGCTGGGCTGTGTCTCATGGCCTGGGCCCTTACCTTTCCCTTGGTGTG
CTCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGT
CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT
TCCAGGTCAAGGCTTACACTTTCAGTGAAACCTTCCACCTGATTGTGTCTATGACTGGCTG
ATCCTCCAAGGTCCAGCCAAGCCAGTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC
CCGGGCTTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC
TGCAGTGGCATCTTCCAGAGCCCTGGTCTTGGGATCCAGAAACAGCATCTGTTGTGGCTAT
CACAGTCCAAGAAGTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG
CAGGAAGCCCCATGACCCCTGAGTTGTGACACAAAGTTGCCCTTGAGAGGTGAGCTGCCCGC
CTCCTCTTCTCTCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCACTACTGGTGTGAGGCAGCCACTGAGG
ACAACCAAGTTTGAAACAGAGCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT
GCTGCACCTCCCACTTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAATGCTCCTGA
GGAGGCCCTTGGGCTCTGCCTCCGCGCCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAACACATG
CAGGATGTGAGAGTCTCTCCTCGGTCACTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA
GAAGCCTGGGACCAAAAGGCTACTGCTGAATAGAAGTAAACAGTTTATCCATGATCTCACT
TAACCAACCCCAATAAATCTGATTCTTTATTTTCTCTTCTGTCTGCACATATGCATAAGTA
CTTTTACAAGTTGTCCAGTGTTTTGTGTAGATAATGTAGTTAGGTGAGTGTAATAAATTT
ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACACAGAATTC
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTAAAGAGAA
CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACA
TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGTTGGGGGATGGTGGGATGT
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCCTAAACATCCTATAATGCACAG
GGCAGTACCCACAAACGAAAAATAATCTGGCCCAAATGTGAGTTGTACTGAGTTTGAGAAA
CCCCAGCCTAATGAAACCCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT
TATCTCTTTCCAGCCTCATTAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGCTATG
GTCTGTTCTTTAGTCTTAGTTTGTATCCCTCAAAGCCATTATGTTGAAATCCTAATCCCC
AAGGTGATGGCATTAAAGAAGTGGGCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC
ATGATTAGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCTTCCACCAT
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAAACAGTGTGCGCAAACCG
ACTCTGTCGTTGCCTTGATCTTGAAGTCCAGCCTCCAGAACTATGAGAAATAAATCTGG
TTGTTTGTAGCCATA

FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594
><subunit 1 of 1, 359 aa, 1 stop
><MW: 38899, pI: 5.21, NX(S/T): 0
MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESCHTEDDLTDAREAGFQV
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRCQAWQDWPLTQVTFYRDGSALGPPGP
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS
PMTLSCQTKLPLQRSAAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ
VWKQSPQLEIRVQGASSSAAPPTLNPAPOKSAAPGTAPEEAPGLPPPPPTPSSDPGFSSPL
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

FIGURE 21

CCCACGCGTCCGCCACGCGTCCGCCACGGGTCCGCCACGCGTCCGGGCCACCAGAAGTT
 TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG
 ATCTTACTGGGCTGCTACTCCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT
 GGAAGTGCACAGAGTGTAAACAGGACCTTGAAAGGGGATGTGAATCTTCCCTGCACCTATG
 ACCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCT
 GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAGTACCAGGGCCG
 CCTGCATGTGAGCCACAGGTTCCAGGAGATGTATCCCTCAAATTGAGCACCTCGGAGATGG
 ATGACCGGAGCCACTACAGTGTGAAGTCACTGGCAGACTCCTGTGGCAACCAAGTCGTG
 AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCCACAGTGACAAC
 TGGCAGCGGTTATGGCTTCACGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC
 GGGGTTCCTCCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACAGGAACCCATC
 AAAGTAGCAACCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA
 TTTCTGCACCTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG
 TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC
 TTGAAAGCAACATCTACAGTGAAGCAGTCCCTGGGACTGGACCACTGACATGGATGGCTACCT
 TGGAGAGACCAAGTGTGGGCCAGGAAAGAGCCTGCTGTCTTTGCCATCATCTCATCATCT
 CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTGCGGAAGACATCCGAA
 CAAGAGCATGTCTACGAAGCAGCCAGGTAAAGAAAGTCTCTCCTCTTCCATTTTGAACCCGT
 CCCTGCCCTCAAATTTTGATTACTGGCAGGAATGTGGAGGAAGGGGGTGTGGCACAGACCC
 AATCCTAAGGCCGGAGGCCTTCAGGCTCAGGACATAGCTGCCCTCCCTCTCTCAGGCACCTT
 CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCCTCTGCTTCC
 AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAGAAATTTAGGCAGAAAGGTTGGGA
 AACCAGGACCACAGCCCCAAGTCCCTTCTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA
 TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT
 CCAGTGATGAGCCAACCTTCCAGAACTCTGGGCAACAACACTACTCTGATGAGCCCTGCATAGGA
 CAGGAGTACCAGATCATCGCCAGATCAATGGCAACTACGCCCGCCTGCTGGACACAGTTCC
 TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTTAAAAATGCCCATTAGGC
 CAGGATCTGCTGACATAATTGCCTAGTCAGTCTTGCCTTCTGATGGCCTTCTTCCCTGCT
 ACCTCTTCTCTGGATAGCCCCAAAGTGTCGCCCTACCAACACTGGAGCCGCTGGGAGTCACT
 GGCCTTGGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGTCTGGATTTGGCTCTGG
 GCCCTTCTAGTATCTCTGCCGGGGCTTCTGGTACTCCTCTCTAAATACAGAGGGAAGATG
 CCGATAGCACTAGGACTTGGTCATGCCTACAGACACTTAATCAACTTTGCCATCTTGCCA
 CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT
 TTCTCTTCTCAGGGCCAGACAGCTTTAATTGAAATGTTATTTACAGGCCAGGGTTCA
 GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTA
 ATCATAACAGC

09978186.101501

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416
><subunit 1 of 1, 321 aa, 1 stop
><MW: 35544, pI: 8.51, NX(S/T): 0
MGILLGLLLGLHGLTVDTYGRPILEVPESVTGPWKGDVNLPCITYDPLQGYTQVLVKNLVQRGS
DPVTIFLRDSSGDHIQQAKYQGRHLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQ
VVRDKITELRVQKLSVSKPTVTGSGYGFTVPQGMRIQLQCQARGSPPISYIWKQQTNNQE
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTMT
YPLKATSTVKQSWDWTDTMDGYLGETSAGPGKSLPVFAILLIISLCCMVVFTMAYIMLCRKT
SQQEHVYEAAAR

Signal Sequence:

amino acids 1-19

Glycosaminoglycan attachment site:

amino acids 149-152

Transmembrane domain:

amino acids 282-300

1997-2000

FIGURE 23

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCACAT
 GGCTGACGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCGTCGGA
 GGCCTCCGGCCGCGCCCGGAGCCAGCAGCAACTGAGCGGGGAAGCGCCGCGTCCGGGGATC
 GGGATGTCCTCTCTCTCTCTCTCTCTGCTAGTTTCTTACTATGTTGGAACCTTGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCATTTCGCCCTGCCACCATCACTGGGGC
 TTCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA
 GTGGTGATCACTTACTCAGTCTGCTACATAAAGTCTGAGTGAAGAACAGAGGGCCG
 AGTGGCCTTTGCTTCCAATTTCTTGGCAGGAGATGCTCTCTGAGATTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTTCAGGGCGCTACGTTGTGGAGCCAT
 GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
 AGAAGGAAGTGACCTGACTTTGCACTGTGAGTCACTCTTGGCACAGAGCCCATTTGTGTATT
 ACTGGCAGCGAATCCGAGAGAAAAGAGGGAGAGGATGAACGCTCTGCCTCCCAATCTAGGATT
 GACTACAACCACCTTGGACGAGTTCTGCTGCAGAACTTACCATGCTCTACTCTGGACTGTA
 CCAGTGCAACAGCAGGCAACGAAGCTGGGAAGGAAGCTGTGTGGTGCGAGTAACCTGTACAGT
 ATGTACAAGAGCATCGGCATGGTTGCAAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG
 ATTTCCTCTTGGTGTGGTGCTAATCCGAAGGAAGACAAAGAAAGATATGAGGAAGAAGA
 GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCGCTCTTGTGAAACCCAGCT
 CCTCTCTCAGGCTCTCGGAGCTCAGCTCTGGTCTCTCTCCACTCGCTCCACAGCAAAAT
 AGTGCTTACCGCAGCCAGCGGACACTGTCAACTGACGACGACCCCGAGCCAGGGCTGGCCAC
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG
 CTAATCTGACCAAAGCAGAAACACACCCAGCATGATCCCGAGCCAGAGCAGGCCTTCCAA
 ACGGCTCTGAATTACAATGGACTTGACTCCACGCTTTCTCAGGAGTCAGGGCTTTTGGACTC
 TTCTCGTCATTGGAGCTCAAGTCACCGCCACACAACAGATGAGAGGTCACTTAAGTAGCA
 GTGAGCATTTGACGGAACAGATTGAGATGAGCATTTTCTTATACAATAACCAAACAGCAAA
 AGGATGTAAGCTGATTCACTGTAAAAAGGCATCTTATGTGCTCTTAGACCAGAGTAAGGG
 AAAGCAGGAGTCCAATCTATTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG
 AGGTGAATATACCTAAAACTTTTAATGTGGGATATTTGTATCAGTGTCTTGAATCACAATT
 TTCAAGAGGAAATGGGATGCTGTTGTAAATTTTCTATGCAATTTGCAAACTTTATGGATT
 ATTAGTTATTGACAGCTCAAGCAGAACCACAGCCTTATTACACTGTCTACACCATGTAC
 TGAGCTAACCACTTCTAAGAACTCCAAAAAGGAACATGTGTCTTCTATTCTGACTTAAC
 TTCATTTGTATAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
 AGAGTGAATGAGTTTCTCCACTCTATCTAATCTCACTATTGATTGAGCCCAAATAAC
 TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTCCATCTTCATGATGTT
 ATGAGGATTGTTGACAAACATTAGAAATATATATGGAGCAATTTGGGATTTCCTCTCAAT
 CAGATGCCTCTAAGGACTTCTGCTAGATATTTCTGGGAAGGAGAAAAATACAACATGTCTATT
 TATCAACGTCTTAGAAAGAAATCTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA
 CCCAACATACATTATAGCTCTCTCTTTCTGAGAAAAATGTGAACACAGAATTGCAAGACTGG
 GTGACTAGAAAGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
 TGGTGCCAGGCACCTGTAGGAAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
 ATTGCACTCCAGCCTGGGTGCAGAGCCGGACTCCGCTCTC

U978183.101504

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLTDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPRVLLQNLMTSYSGLYQCTAGNEAGKESCVVRVTQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEEPNEIREDAEAPKARLVKPPSSSSSGSRSSRSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

09978183-103501

FIGURE 25

GTCGTTCCCTTGTCTCTCGCGCCAGTCTCTCCCTGGTTCTCCTCAGCCGCTGTGCGAGGAGAGCACCCGGA
 GACGCGGGCTGCAGTGCAGCGGGCTTCTCCCGCTGGGCGGCTCTCGCGCTGGGCGAGGTGCTGAGCGCCCCTAG
 AGCCTTCCCTTGGCGCTCCCTCTCTCGCGGCCGAGCAGTGCAATGGGGTGTGGAGGTAGATGGGCTCCCG
 GCCCGGGAGCGGGGTGGATGCGCGCTGGGCGAGGAGCCGCCGATTCAGCTGCCCGCGCGCCCGGGGCG
 CCGCTTGGCTCCCCGTTACGCCATGGGGAGCTCTCCGAGCAGCAGCACCGCCCTCGCTCTCTGCACCGCATC
 CGCCCGCGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCTGCTTGGATTCCTTAGGACCAACACAGCTCAG
 CAGAACAGAGGGCTCGAATCTCATTTGGCACATACCGCCATGTTGACCGTGCACCGGGCAGGTGCTAACTGT
 GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTTGACCAACACAGGCTTGGCGCTCTGCGAGGTGGCCCT
 GTGGGGAGCTTTACAGGCATGAGAAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCATG
 ATTGAGAAATTTACTTGTGTGCTTGTACTGACCGAGAAATGCACTTGCACCTTGGCATGTTCACTGTTAAAGCT
 CCGTGTGCCCGCCATACGGTGTGCTCTGTGGGTGGGGTGTGCGGAAGAAAGGAGAGACTGAGGATGTGCGG
 TGTAAAGCAGTGTGCTCGGGGTACTTCTCAGATGTGCTTCTAGTGTGATGAAATGCAAGCATACACAGACTGT
 CTGAGTCAGAACCTGGTGTGATCAAGCCGGGACCAAGGAGACAGACAACTCTGTGGCAGCTCCCGTCTCTC
 TCCAGCTCCACCTCACTTCCCCGGCACGCCATCTTCCAGCGCTGAGCAGCATGGAAACCATGAAGTCCCT
 TCTCCACTTATGTTCCCAAAGGCATGAACCTCAACAGAACTCAACTCTTCTGCTCTGTTAGACCAAAGTACTG
 AGTAGCATCCAGAAAGGACAGTCCCTGACACACAGCTCAGCAAGGGGAGGAAGAGCTGAACAGACCCCTC
 CCAAACCTTCAGGTAGTCAACACAGCAAGGCCCCACACAGACACATCTGTAAGCTGCTGCGCTCCATGGAG
 GCCACTGTGGGGCGAGAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCTTAGACAGAACCTTACACAG
 GATTTTGAACATCAATGACATTTGCCCTGGATGATTGTGCTTTTCTGCTGTGGTGTGTTGTGTGATTGTGGTG
 TGCACTATCCGGAAGAGCTCGAGGACTTGAAAGAGGGGCCCGCGAGAGTCCAGTGCATTTGCGAAAGAGGCA
 GGGCTGAAGAAATCTCATGACTCAACCCAGAACCGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCTGAT
 ATCCCTGAAGCTGTGAGCAGCCAGTGGGAGCCAGTGGGAAAGATATCTATCAGTTCTTTTGCATGCCAGGTGAG
 AGGGAGGTGCTGCTCTTCCAAATGGGTACACAGCCGACACAGCGGGCTTACGCACTCTCTCAGCACTGAGACC
 ATCCCGCGCCCGGAGCCAGCTCGCCAGCTAATTAGCGCCCTGCGCCAGCACCGAGAAACAGATGTTTGTGGAG
 AAGATTGTGGGCTGATGAGAGACACCAACAGCTGGAATCTGACAACTGTGCGATGAGGCTCCAGCGCG
 CTAGCCCGAGCCCATCCCAAGCCCAACGCGAACTTGAAGATTCGCTCTCTGAGCGGTGGAGCTTCCCCA
 CAGGACAAAGACAAAGGCTCTTCTGTGATGAGTGGAGCCCTTCTCGCTGTGACTCTACATCAGCGGCTCC
 TCCCGCTTGAGCAGAACGCTTCTTTATTAACAAAGAAAGAGGACAGACTGTGCGCAGGTACGCTGAGAC
 CCGTGTGACTTGCAGCTATCTTTGATGACAGCTCCTTCTCAATCTGAGGAGCTCGGGGTGATTGAAGAG
 ATTCCCGAGCTGAGGACAAACTAGACCGCTATTGGAATTAITGGAGTCAAGAGCCAGGAGCCAGCCAGACC
 CTCTGGAGCTGTGTTATAGCCATCTCCCTGACCTGCTGTAGAACATAGGGATATCTGATTCTGGAATTAATCA
 ATTTAGTGGCAGGGTGGTTTTTAAATTTCTTCTGTTTTGATTTTTTGTGTTTTGGGGTGTGTGTGTTTTGT
 GT
 TCTCTCTCTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTATAAGCTTTTGGCAGGTGTAACCTGTTGTGA
 ATACCCACCACTAAAGTTTTTAAAGTTCATATTTTCTCATTTTGCCTTCTTATGTATTTTCAAGATTATCTG
 TGCACTTTAAATTTACTTTAATCTTACCATAAATGCAAGTGTGACTTTCCACACACTGGATTGTGAGGCTCTTAAC
 TTCTTAAAGATATAATGGCATCTGTGAATCCTATAAGCAGTCTTATGTCTCTTAACATTTACACCTTACTTTTT
 AAAAACAAATATTATTACTTTTTTATTATTGTTTGCCTTTATAAATTTTCTAAAGATTAAAGAAATTAAGA
 CCCCATTGAGTTACTGTAAATGCAATTCACCTTGAAGTTATCTTTAAATATGTCTTGTATAGTTATATTTATG
 CTGAAATCTGACCACTATTGCTGATTGTATGGTTTTACCTGGACACCGGTAGATGCTTGTATTACTTGTATC
 TCTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCATTCAAGATTGCTATTTAAAGTGGCTT
 GACACTGGGCGCCAAAGAACTTGAACCTTCACTTTTAGGATTTAGAGTGTGTTGGAACACATTGCTGCACTT
 GGAAAGTCAAAATCAAGTGCAGTGGCGCCCTTCCATAGAGAATTTGCCAGCTTTGCTTTAAAGATGCTCTTG
 TTTTTATATACATAAATCAATAGGTCCTCACTGCTCTCAAGCCCTGTGCTGAGGATTCTCTTCAACAAAT
 ACTTTAATTAATAATGGCTGCAACTGTAAAGACCTTGTCTGATATTTGACGATGCTGCCATTTTCAAAATG
 TACCTTCTAAGTCTAGTGGCAGCTTCCAATGCAAGGTGGCGTGAAGTCCCTTTGTGTGGGTGGGGTGTGGT
 GTAGTGTGTGAAGGACGATATCAGAAAAATGCTTCAAGTGTACTAATTTTATTAATAAACATTAGGTGTTTGTTA
 AAAAAAAA

09978188-101501

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><subunit 1 of 1, 655 aa, 1 stop
```

MGTPSSSTALASCSCRIARRATATMIAGSLLLLGLFLSTTTAQPEQKASNLIGTYRHVDRATG
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTPTTRHENGIEKCHDCSQPCPWPMEIKLPCA
ALTDIRECTCPPGMFQSNATCAPHTVCPVGWGVRRKGTETEDVRCKQCARGTFSDVPSSVMKC
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVNVHQGPHHRHIL
KLLPSMEATGGEKSSPTIKGPKRGHPQRNLHKHFDINEHLPMMIVLFLLLVLVVIIVVCSIRK
SSRTLKKGPRQDPSAIVEKAGLKKSMPTPTQNRKWIYYCNGHGIDILKLVAQVGSQWKDIY
QFLMNETSEREVAAFNSNGYTADHERAYAAQHWITIRGPEASLAQLISALRQHRNRNDVVEKIRG
LMDETTQLETLKRLGLMSPSPPLSPSPISPNAKLENESALLTVEPSPQDKNGFFVDESEPLL
RCDSTSSGSSALSRLNFSFITKEKDDTPSRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ
AEDKDLRDLFEIIGVKSQEASFTKDLDSVYSHLPDLL

amino acids 1-41

amino acids 350-370

FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCGTTGGTGCATCTACATTTTGGGA
CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCAC
CATGGGGGAAATGATCCGCTGCTGTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTGGCC
TTGATGATTTGAAATAAGTCCTGTTGCACAGATGCAGATGCTGTTGCTGCACAGATCCTG
TCAGTCTGCCATTGAAGTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT
TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAAGACGGGGAGGAC
GAGTACCGCTGTGTCGGGTGGTGGTCAGAATGCCGTGCTCCAGGTGTTACAGCTGCTTC
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAATGTTGCCTGTGCCAAC
TGGGTTTTCCCAAGCTATGTGAGTTTCAAGTAACTCAGAGTGAGCTCGCTGGAGGGGAGTTT
CGGGAGGAGTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA
CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCAGTGCAAGCCT
GTGGTCATAGAAGGGGCTACAGCTCACGCATCGTGGGTGGAAACATGTCTTGTCTCTCGCAG
TGGCCCTGGCAGGCCAGCCTTCAAGTCCAGGGCTACCACTGTGCGGGGGCTCTGTATCATC
GCCCTGTGGATCATCACTGCTGCACACTGTGTTTATGACTTGTAACCTCCCAAAGTCATGGA
CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAG
ATTGCTTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT
GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCTGCCAACTCTGAAGAGA
ACTTCCCCGATGGAAAAGTGTGCTGGACGTCAAGATGGGGGGCCACAGAGGATGGAGGTGAC
GCCTCCCTGTCTTGAACACGCGGCCGTCCCTTTGATTTCACAACAGATCTGCAACACAG
GGACGTGTACGGTGGCATCATCTCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG
TGGACAGTGCACAGGGGACAGCGGGGGCCCCCTGGTGTGTCAAGAGAGGAGGGCTGTGGAAG
TTAGTGGGAGCGACAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACAC
CCGTGTCACTTCTTCTGGACTGGATCCAGGACGATGGAGAGAGACCTAAAAACCT**TGAA**
GAGGAAGGGGACAAGTAGCCACCTGAGTTCCTGAGGTGATGAAGACAGCCCGATCCTCCCT
GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCCTTGGAGCTCTGAGTTCGGGCACCA
GTAGCAGGCCCCGAAAAGAGGCACCCTTCCATCTGATTCCAGCACAACTTCAAGCTGCTTTT
GTTTTTTGTTTTTTTGGAGGTGGAGTCTCGCTCTGTTGCCAGGCTGGAGTGCACTGGCGAAA
TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAGCGATTCTCTGCTCAGCTTCCCCA
GTAGCTGGGACCACAGGTGCCGCCACACACCCAACTAATTTTTGTATTTTGTAGTAGAGAC
AGGTTTACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT
CAGCCTCCACAGTGTGGGATTACAGGCATGGGCCACACGCCTAGCCTCAGCTCCTTTC
TGATCTTCACTAAGAACAAAGAGACAGCAACTTGCAAGGGCGGCCTTCCCACTGGTCCAT
CTGGTTTTCTCTCAGGGTCTTGCAAAATTCCTGACGAGATAAGCAGTTATGTGACCTCAG
TGCAAGCCCAACACGCCACTCAGAAAAGACGACCCAGCCAGAAGTGCAAGACTGCAGTC
ACTGCAGTTTTTCTCTAGGGACCAAGAACCAACCCACCTTTCTACTTCCAGAGATTAT
TTTTCATGTGGGGAGGTTAATCTAGGAATGACTCGTTAAGGCCCTATTTTCAAGTATTCTT
TGTAGCATTTGGTGCTTGACGTATTATTGCTCTTGATTCAAATAATATGTTTCTTCCCT
CATTGTCTGGGTGTCTGCGTGACTGGTGACGTGAATCAAATCATCCACTGAAA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVVRVGGQNAVLRVFTAAAS
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIHLLPDDKVLTALHH
SVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT
PLWIIITAAHCVDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHR
DVGGIISPSMLCAGYLTGGVSDCQGDSCGGPLVCQERRLWKLVGATSPGIGCAEVNKPVGVT
RVTSFLDWIHEQMERDLKT

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624
><subunit 1 of 1, 735 aa, 1 stop
><MW: 80177, pI: 7.08, NX(S/T): 5
MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVSASVRSGLWIPVKSFDSK
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCYYHGHVRG
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLA
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGDLEKVKQRLIEIANHVDKF
YRPLNIRIVLVGVEVWDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFGMNHDTLDRGCSCQMAVEK
GGCIMNASTGYPPFMVFSSCSRKDLETSLKGMGVCLFNLPEVRESFGGQKCGNRPFVEEGEE
CDCGEPEECMNRCNATTCITLKPDAVCAHGLCCEDCQLKPAGTACRDSNSCDLPEFCTGAS
PHCPANVYLHDGHSCQDVGDCYNGICQTHEQQCVTLWGPGAKPAPGICFERVNSAGDPYGN
CGKVS KSSFAKCEMRDAKCGKIQCGGASRPVIGTNAVSIETNIPLQQGGRILCRGTHVYLG
DDMPDPGLVLAGTKCADGKICLNRCQNISVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP
FCDKFGFGGSTDSGPIRQAEARQEAAESNRERGGQGEPEVGSQEHASTASLTLLI

Signal peptide:

amino acids 1-28

0070101501

FIGURE 31

TCCCAAGGCTTCTTGGATGGCAGATGATTTNTGGGGTTTTGCATTGTTTTCCCTGACAACGAAA
ACAAAACAGTTTTTGGGGGTTT CAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA
AGAGGACTCAAAAAGTTTTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT
GGGCCCAGTGTCCTTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNINT
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATATATGAAAAATAGCAGGGTTTT
AGTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

09073108.101501

FIGURE 32

CATCCTGCAACATGGTGAAACACGCCTGGCTAATTTTGTGTATTTTGGTAGAGATGGGA
TTTCACCGTGTTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCGCCTCGGCCTCCC
AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCCGGCCACAACTTTTAAAGAAGTTAAT
GAAACCATACCTTTTACATTTTAAATGACAGGAAAATGCTCAATAAATGTGTTAACCCAAA
TTCTGGATACAAAAGTACAATCTTTACTGTGTAATACATGTATATGTAATATGAAAATA
TACCAAAATATCAATAATACTTATCTCTGGGTAAAAACCTCTTCTCATACCTGTGCTAACAA
CTTTTAACAAAAAAATTTGCATCACTTTTAAAGATCAAGAAAAATTTCTGAAGGTATATGGG
ACAGAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAGATTGAAATCTGCCT
TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTTCTAAGCAACTTAAATGTTTGTTCGA
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGAGTGATGTCACTGCCATTATGATGCCCC
TTGAATATAAGACCTTACTTGCTATCTCCCTGCACCAGCCAGGACCCATCTCCAGC
ACACTGAGCAGCAAGCTTGGACACACGGCACACTGATCCAAATGGGTAAGGGGATGGTGCGA
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCGTGCAGGTTTCTTCATTGT
CCTTTAACAGTATGCCGGAAGCTACTGCAGCCGAAACCACAAAGCCCTCCAACAGTGCCCT
ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCATTAAAGAGG
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACACTAAAACCGAATCCAAATGGTGCCT
AGAAGTTCAATGTGGCAAGGAAAAAAACCAGGTCTTCATCAAATCTACTAATTTCACTCCTT
ATTAACAGAGAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTAAAGAGCATCTGAAGGATTT
GACTAGATGATAAATGCCTGTACTCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG
AGGTGAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA
AATATGACTGGGCGTGGTGGTGAAGTGCCTGTGATCCAGCTACTCAGGTGGCTGAAGCAGG
ACAATCACTTGAACCTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAAAAGCCAAGTGCAAGTGGCT
CACGCCTGTAATCCCGGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAGGAGATCA
AGACCATCTGGCTAATACAGTGAAACCTGTCTCTACTAAAAATACAAAAAATTAGCCGGG
GATGTTGGCAGGACCTGGAGTCCCAGTACTCGGGAGGCTGAGGCAGGAGAATAGCGTGAA
CTCAGGAGGCCGAGCTTGCAGTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG
CGCGAGCTCCGTCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 33

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVLLAL

LHLVH

Signal peptide:

amino acids 15-27

09978188.10501

FIGURE 35

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47629, pI: 5.90, NX(S/T): 0

MPARPGRLPLLLARPAALTALLLLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS
KHLTYADMFTHGIQSAAHFVMFFAPWCGHCQRLQPTWNLDGDKYNSMEDAKVYVAKVDCTAH
SDVCSAQGVRGYPTLLKLFKPGQEAVKYQGPRDFQTLNWLQTLNEEPVTPEPEVEPPSAPE
LKQGLYELASNFELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT
QHYELCSGNQVRGYPTLLWFRDGGKVDQYKGRDLESLEYYVESQLQRTETGATETVTPSEA
PVLAAEPEADKGTVLALTENNFDITIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICSKYSVRYPTLLLFRRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL

Signal sequence:

amino acids 1-32

00078133-101501

U.S. DEPARTMENT OF AGRICULTURE

CTTTTCTGAGGAACCCAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTCA
CCGCTGAAGTCTGTGCCACACACACAATTCACCAGGACCCAAAGGAGATGATGGTGA AAAA
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGA
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGCAAACTGGATATTAGTATTGCTCGGCT
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAACTGAAGAGAAAT
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAAGGATTTCG
GGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC
CAAGAGTGGCTTCTTTGCGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA
TGTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAAACCCAGCGAC
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG
CCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT
ACGTATTTTGACTATTTTCTGTGACCGCTCATTACAGTTATTGTTATCCATCCTTTTTTCTG
ATTGTACTACTATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT
CCATCATCAAAAAAATAAAAAA

FIGURE 37

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

MNGFASLLRRNQFILLVLFLQLQISLGLDIDSRPTAEVCATHTISP GPKGDDGEKGD PGEEG
KHGKVGRMGPKGIKGELGDMGDQGNIGKTGP I GKKGDKEKGLLG I PGEKGKAGTVCDGGRY
RK FVGQLDISIARLKTSMKFVK NVIAGIRETEEFYYIVQEEKNYRESLTHCRIRGGMLAMP
KDEAANTLIADYVAKSGFFRVF IGVDL EREGQYMSTDNTPLQNYSNWNEGEPSDPYGHEDC
VEMLSSGRWNDECHLTMYFVCEFIKKKK

Signal peptide:

amino acids 1-25

FIGURE 38

GGTTCATATCGATTGGAATTCGGCCCACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCTGCTCTCCGCCGTGTGGAGTGGTGGGGGCTGGGTGGGAATGGGGCGTGT
GCCAGCGCACCGCGCTCCTTGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTT
CGGAAGGGAGGATCAGGGATGTTTGCAGAGCGGTGGAACGACCGTGCCGATAGAGGAAGC
GGGCTCCATGGCTGCCCTCTGCTGCTGCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA
AGCTACACCTCTGGCCGAGTTTGGCTTGGCTTCCGGCGGACTTGGCCCTTTGCGGTGCGAGCT
CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCGACCCGGAAG
TCCCGAGGGGGGCTGCAGCTTGGCTTGGCGCTCGCGGAATGGCCGAGCGCGCCGCGCG
ACACCTTTCTCATTACAGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC
AGGGCTGCACGCGCCTTCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGCGCGCGACAG
CGCGCAGGGGAGCGCTGGAGAAGGCGAGCGGCGAGCGCGGAGCCGAGATGCAGCGGCCG
GAAGCGCGCGGAGTTTGCAGGAGGGGACGGTGC CGCAGAGGTGGAGGAGCGCGCGCCCT
CTGTCACTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCAGAGTTTCTGTGGCTCTG
GTTGGGCTGGCCAAAGGCGCGCTGCGCACTGCTTTGTGCCACCGCCCTGCGCCGGGGCC
CCCTGCTGCACTGCTCCGAGCTGCGGCGCGCGCGCGCTGGTGTGGCGCAGAGTTTCTG
GAGTCCCTGGAGCGGAGCTGCCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGCTGAGG
CCGAGGAACCCACCTCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG
GGCCAGTGCCAGGATACCTCTCTTCCCCCAGAGCATAACAGACACGTGCTGTACATCTTC
ACCTCTGGCACCAAGGGCTCCCCAAGGCTGCTCGGATCAGTCACTGAAGATCCTGCAATT
CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCAC
TCTACCAATGTCCGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTG
GTGCTGAAATCCAAGTTCTCGGCTGGTCAAGTTCTGGGAAGATTGCCAGGACGACAGGGTGAC
GGTGTTCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACAGCCCCGAGCAAGGCGAG
AAGCTGGCCATAAGGTCCGGCTGGCAGTGGGCGAGCGGGCTGCGCCAGATACCTGGGAGCGT
TTTGTGCGGCGCTTCCGGCCCTGCGAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT
GGCCACCATCAACTACACAGGACAGCGGGGCGCTGTGGGCGTGTCTCTGGCTTTACAAGC
ATATCTTCCCCTTCTCCTTGATTGCTATGATGTCAACAGGAGAGCCAATTCCGGACCCC
CAGGGGACCTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGCTAAGCCA
CGAGTCCCCATCTCTGGCTATGCTGGCGGGCCAGAGCTGGCCAGGGGAAGTTGCTAAAGG
ATGTCTTCCGGCTGGGGATGTTTCTTCAACACTGGGACCTGCTGGTCTGCGATGACCAA
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC
CACAAACGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGACGCTCTATG
GAGTCACTGTGCCAGGGCATGAAGGAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC
CAGCTTTGGACCTTATGCAGCTCTACACCCAGCTGTCTGAGAATCTGCCACCTTATGCCCG
GCCCCGATTCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAACAGCAGCAAG
TTCGATGGCAATGAGGGCTTCGACCCAGCACCCTGTCTGACCCACTGTACGTTCTGGAC
CAGGCTGTAGGTGCTTACCTGCCCTCACAACTGCCCGGTACAGCGCCCTCTGGCAGGAAA
CCTTCGAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGGAACCTGTGGGGTGGGG
CCGTTGACAGGTGTACTGGGCTGTGAGGGATCTTTTCTATACCAGAACTGCGGTCACTATTTT
GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTGTGACCTAAAAAATAAATAAATAA
AAAAAATAAAGGGGCGCGACTCTAGAGTGCACCTGCAGTAGGGATAACAGGGTAATAAGC
TTGGCCCGCATGGCCCACTTGTTTATTGACG

FIGURE 39

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913
><subunit 1 of 1, 730 aa, 1 stop
><MW: 78644, pI: 7.65, NX(S/T): 2
MGVCQRTAPWKEKSQLERAALGFRRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLLPL
LLLLKLHLWPQLRWLPADLAFVRLCCKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQ
RAAHTFLIHGSRFFSYSEAERESNRAARAFRLRALGWDWGPDPGGDSGEGSAGEGERAAPGAGD
AAAGSGAEFAGGDGAARGGGGAAAPLSPGATVALLLPAGPEFLWLWFLAKAGLRTAFVPTAL
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA
EVDGFPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL
ALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRTVVFQYIGELCRYLVNQPP
SKAERGHKVR LAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW
LYKHIFPFSILIRYDVTTEGPIRDPQGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPELAQGK
LLKDVFRPGDVFFNTGDLVLCDDQGFLRFHRTGDTFRWKGENVATTEVAEVFEALDFLQEV
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTETFK
QQKVRMANEGFDPSTLSDPLYVLDAQAVGAYLEPLTTARYSALLAGNLR I

Type II transmembrane domain:

amino acids 45-65

Other transmembrane domain:

amino acids 379-398

cAMP- and cGMP-dependent protein kinase phosphorylation site
starting at amino acid 136

CUB domain protein motif

amino acids 254-261

putative AMP-binding domain signature

amino acids 332-343

N-glycosylation sites

amino acids 37-40 and 483-486

FIGURE 40

CCTGTGTTAAGCTGAGGTTTCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA
CACATCCCCAAGAACCTCGAGCTCACACCAACAGACACACGCGCATACACACTCGCTCTC
GCTTGTCCATCTCCCTCCCGGGGAGCGCGCGCGCTCCACCTTTGCGGCACACTCCGGC
GAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGAACCTCGGATTGCGACTCTGAACCC
CCATGTGTGTTTAAACACTTCTTTCCCTTCTCTTCCCTGTTTGAATTGACCGGTTTCCA
TCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCAGCCAGCCCTTGTGGCTTGGCATCGT
CCATCTGGCTTATAAAAGTTTGTGAGCGCAGTCCAGAGGGCTCGCTGCTCGTCCCCTCGG
CTGGCAGAAAGGGGTGACGCTGGGGCAGCGCGAGGAGCGCGCGCTGCTTGGCGGGCTTT
CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCCGTGGGGTTTACCGAGCTGGATTGTATG
TTGCACCATGCTCTTGGATCGGGGCTGTGAATCTTCCCCTCTTGGGGCTGCTGCTCTCCC
TCCCCGCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCGCGCAGGCGTACGGTGCC
AAGGGATTAGCCTGGCGGACATCCCTACCAGGAGATCGCAGGGGAACACTTAAGAACTCTG
TCCTCAGGAATATACATGCTGCACCAAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAC
TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTTGTGCGCACCACCTTTTGTGTCAGG
CATAAGAAATTTGACGAATTTTCCGAGAGCTCCTGGAGAAATGAGAAAGTCACTAAATGCA
TATGTTTGTACGGAATCTTGGCATGCTGTACATGCAGAAATCGACAGGACTTCCAGGACTCT
TCACAGAGCTGAAAAGGTACTACACTGGGGGTAAATGTGAATCTGGAGGAAATGCTCAATGAC
TTTTGGGCTCGGCTCCTGGAACGGATGTTTTCAGCTGATAAACCCCTCAGTATCACTTCAGTGA
AGACTACCTGGAATGTGTGAGCAATACTAGACCACTCAAGCCATTGGAGACGTGCCCC
GGAAACTGAAGATTAGGTTACCGCGCCTTCAATGCTGTCGAGGACCTTGTCCAGGGGCTG
ACTGTGGGCAGAGAAGTTGCAACCGAGTTTCCAAGGTCAGCCCAACCCAGGGGTGATCCG
TGCCCTCATGAAGATGCTGTACTGCCCATACTGTGCGGGGCTTCCCACTGTGAGGCCCTGCA
ACAACACTGTCTCAACGTCATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG
TGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGCATGGAGGGGCCATTCAACAT
TGAGTCGGTCATGGACCCGATAGATGTCAAGATTCTGAAGCCATTATGAACATGCAAGAAA
ACAGCATGCAGGTGCTCTGCAAGGCTTTTCAGGATGTGGTCAGCCCAACCTGCTCCAGCC
CTCAGATCTGCCCGCTCAGCTCTCGAAAATTTAATACAGTTTCAGGCCCTACAATCCTGA
GGAAAGACCAACAACTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGACATAAAGAGA
AATTGAAGCTCTCTAAAAAGGTCTGGTCAGCATTACCTTACACTATCTGCAAGGACGAGAGC
GTGACAGCGGGCAGCTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT
GCCTGAGATCATGAATGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACA
TCACTCGGCTGACACTTTTATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAA
CTAAAAAAGCCTACAAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG
CTCAGGGAGTGGCAGTGGTGTCATGGATGACGTGTGTCCTCCACGAGTTTGAAGTTTGTACCA
CAGAGGCCCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTTTCGACGCCACAGCTGGC
CACTCCCTGCTCTCCTGGTCTCTCACCTGCATTGTCTGGCACTGACAGAGACTGTGCAGATA
ATCTTGGGTTTTTGGTCAGATGAAACTGCATTTAGCTATCTGAATGGCCAATCACTTCTT
TTCTTACACTCTTGGCAATGGACCATGCCACAAAACCTTACCGTTTTCTATGAGAGAGAGAG
CAGTAATGCAATCTGCCTCCCTTTTGTTTTCCAAAGAGTACCGGGTCCAGACTGAACTG
CTTCTCTTCTTCTCAGCTATCTGTGGGACCTTGTTTATCTAGAGAGAATTTCTACTCA
ATTTTTCGTACCAGGAGATTCTTACCTTATTGCTTTTATGCTGCAGAAGTAAAGGAAT
CTCAGGTTGTGAGGTTTTTTTTTCTCATTTAAAT

FIGURE 41

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914

><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

MPSWIGAVILPLLGLLLSLPAGADVKA RSCGEVRQAYGAKGFS LADIPYQEIAGEHLRICPQ
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKSLNDMF
VRTYGMLYMQNSEVFQDLFTELKRYT TGGNVNLEEMLNDFWARLLERMFQLINPQYHFS EDY
LECVSKYTDQLKPFQDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAERLEGGPFNIES
VMDPIDVKISEAIMNMQENSMQVSAKVFGCGQPKPAPALRSARSAPENFNTRFRFPYNPEER
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPTYICKDESVTAGTSNEE ECWNGH SKARYLPE
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG
SGSGCMDDVCPTFEFEFVTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

Signal peptide:

amino acids 1-23

0070103 10101

FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCGAAAGAAGCTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAAAGCGCAG
 CAGTTTGCAGCGCTTCGCGCCGGGTGCGCACTACGCAAGACCAAGCGGGCTCCGCGCGGACCGGCGCGGGGGC
 TAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAGGAATTCGTGCCCGGAGTTTCTCGGAGGT
 GGAGGGAGATCAGGAAACGGCTTCTTCTCACTTCGCGCGCTGTGTGAGTGTCTGGGAGAGATTGGCAAACCGCTTAGG
 AAAGGACTTGGGAAATAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCCGTCCACTACGCGAGTTTATCTG
 TCTGATCAGAGCCAGACGCGACGCGTCCACTTCGCAAGTTCTTTCCAGGTGTGGGGACCGCAGGACAGACGCGCGA
 TCCCGCGCCCTCCCTACGACACTCCGAGGAGTCAAGCTCGCTCCCAACGTCGAGGGCGCTCTGGCCACGA
 AAAGTTCCTGTCCACTGTGATTCTCAATTCCTGTCTGGTTTCTTCAGAGAACTTTGGGTGAGATATTA
 ACTTTTTCTTTTTTTTTTCTTGGTGGAAAGTGTCTTAGGGAGGGGGAGGAGGAGGAGAAAGTGAATGTGC
 TGGAGAAGAGCGAGCCCTCCTGTGTTCTTCGAGTCCCATTAAGCCATCACTTCTGGAAGATTAAAGTTGT
 CGGACATGGTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTCAACGCTGTTGGGTGCATG
 TGTGCGCCGCGAGCGGCGGGGCGCGTGGTTCTCCGCGTGGAGTCTCACTGGGACCTGAGTGAATGGCTCCCA
 GGGCTGTGCGGGGCATCCGCTCCGCTTCTCCACAGGCGTGTGTCTGCTGGAAAGTGTGAGCAATGGGG
 CGCTGGCAGGATTTCTGGATCCTCTGCTCCTCACTTATGGTTACCTGTCTGGGGCCAGGCTTAGAAGAGGAGG
 AAGAAGGGGCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCGAGCAACACTTCCACCTCCGAGCCCATCTCA
 TTTTCATCTAGCCGATGATCAGGGATTTAGAGATGTGGTTTACCAGGATCTGAGATTAAACACCTACTCTGT
 ACAAGCTCGCTCGCGGAGGAGTTAAACTGGAGAATCTACTATGTCAGGCTATTGACACCATCCAGGAGTCAGT
 TTATTACTGGAAGATATCAGATACACCGGACTTCAACATTCTATCATAAGACCTACCCAAACCAACTGTTTAC
 CTCTGGACAATGCCACCTTACCTCAGAACTGAAGGAGGTGTGATATTCAACGCATATGGTCGGAATGGCACT
 TGGGTTTTAAAGAAAAGATGCATGCCACCAGAAAGAGGATTGATACCTTTTGGGTTCCTTTTGGGAAAGT
 GGGATTACTATACACTCAAAATGTGACAGTCTCGGGATGTGTGGCTATGACTTGTATGAAAACGACAATGCTG
 CCTGGGACTATGCAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTTAGCTTCCGATA
 ACCCCACAAAGCTTATATTTTATATACTGCCATCAAGCTGTTCATTCAACACTGCAAGCTCCTGGCAGGTATT
 TCGAACACTACCGATCCATATCAACATAAAGCAGGAGAAGATATGCTGCCATGCTTCTGCTTAGATGAAGCAA
 TCAACAACGTGACATTTGGCTCTAAGACTTATGGTTTCTATAAACAACGACATTTATCAATTTACTCTTCAGATAATCT
 GTGCGCAGCCTACGGCAGGAGGGGTAACCTGGCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC
 GGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTGAAGGAACCTGTGCAATCACTG
 ACTGTTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT
 GGGAGACCATAAAGTGAGGGTCTTCGCTCAACCCGAGTAGATATTTTGCAATCAATTGACCCCTATACCAACAGCG
 AAAAAATGGCTCTGGGACGACAGGCTATGGGATCTGGAACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG
 GAAATGTCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTGAGCAACCTGGGACCGAACC
 GTGGCAATGAACGGATCACCTTGTCACTGGCAAAAGTGTATGGCTTTTCAACATCAGACCGACCCATATGA
 GAGGTTGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCAGATTCAACAAAAC
 TGCAGTCCGGTCAAGTATCCCCCAAGACCCAGAAAGTAAACCTTAGGCTCAATGGAGGGGTCTGGGGACCATG
 GTATAAAGAGGAAACCAAGAAAAGAACGCAAGCAAAAACTAGGCTGAGAAAAAGCAAAAGAAAAGCAAAAAA
 GAAGAAGAAAACAGCAGAAGCAGTCTCAGGTAACCCAGCAAAATTTGGCTCGATAATATCGCTGGCTTAAGCGTCA
 GGCTGTGTTTCTGCTGTGCCACTCCAGAGACTTCTGCCACTGGCCGCCCACTGAAACCTGTCTGCTCAGTG
 CCAAGTGCTACTCTTGCAAGCCCACTTAGAGAGAGTGGAGATGTTTATTTCTCTGCTCCTTTAGAAAAAGCTG
 GTGAGTCTGAGTTCACCTGTGCTGTGCTCAGTCACTGACCAAACTGCTTTGAATATAGGAGGAGAACATA
 ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAAACTACCTTTGATAAATTAC

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FIGURE 42B

AGTCAAAGATTGTGTACCTCAAAGCCCTGAAGAATATATTTTCTGGTGAATTTTGTATGTCTGTATATGA
CACTTGGGTTTTTTAAATAATTCTATTTTATATATATAAATATATGTTTCTTTCTGTGAAAAGCTGTTTTCT
CACATGTGAACAGCTTGACCTTCATTTTACCATGCGTGAGGGAATGGCAAAATGAAGATGTTTGGAGCACTGCC
ACAATGAATGTAACATATTTCTAAACACTTTACTAGAGAACATTTTCAGTATAAAAAACCTAAATTTATTTTACA
GAAAAATATTTTGTGTTTTTATAAAAAAGTTATGCAAAATGACTTTTATTTTATTTCTGTCATACCATTAGAAGA
ATTTTATTTTCATTTCTTCAAATATCAAGCACTGTAATACTATAAATTAAGTAATACIGTGTGAATTGAGACTA
TAAAAAACATCATTCAGAAAACCTTTATAATCGTCATTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT
ATTACTTGGAAATTCATGTTTGTGCGAGTTGAGACAACCTTATGTTTCTATCATAACTATTTATGTATCTT
AATTATTAAGATGATTTACTTTATGGCACTAGAAAAATTTACTGTGGCTTTTCTGATCTAACTTCTAGCTAAAAAT
GTATCATTTGGTCTAAAAAATAAAATCTTTACTAATAGGCAATTGAAGGAATGGTTTGTCTAACCAACCAAGTAA
TATAATATGATTTTACAGATAGATGCTTCCCTTGGCTATGACATGGAGAAAAGATTTTCCATAATAATAACTAA
TATTATATTAGGTTGGTGCAAAACCTAGTTGGCGTTTTTCCCATTAAGTAATAACCTTACTCTTATACAAAGT
GGACACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCGCTGGAGTAGGTAACCTTGCTTGGAAACCCC
ACATGCAAAAGCTCATGAGGAGAAATTAAGGAGTATTTATCAGTAATGAAGTTTATCATGGGTCATCAATGAGCATA
GATTTGGTGTGGATCCTGTAGACCTTGGTGTTTCTTTGAAGTGCCCTCTCCTAATGCAGAGGCCCTGAAGCTTAC
AGTATACACTTGAAGAGTCACAGATAGCTAGAAATATGATCTTTGAAGTTATAACTGTGATCTGAAAATGTGTGT
GGTGGTATGACAGCATACCATTAATAATACATTTACATCACAGCTCAAAGGACTGTGATATAATCCATTTATATCAC
AACTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAATGTATAAAGAATCTATAAT
CTAGTACTGAAATTACTAAATGGGTAAGATGATTTAAATGATTTTAAATTTTACATTTTATTTCTAGAAATATAT
GGCTCCATTTTATTTTATAGTGTAAAGTTGTATTTCTTAAAGTTTGTGTTTGTGCGACAGTATCTTTTAAATGAG
TCTTAAAAATAAAGGCATATTTTCATGTTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AA

0978103 11501

FIGURE 43

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296
><subunit 1 of 1, 515 aa, 1 stop
><MW: 56885, pI: 6.49, NX(S/T): 5
MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTGYGLSWGQALEEEEEEGALLAQA
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYHGSEIKTPTLDKLAAEGVKLENYYVQPICTP
SRSQFITGKYQIHTGLQHSIIIRPTQPNCLPLDNATLPQKLKEVGYSTHMGKWHLGFNKKEC
MPTRRGFDTFPGSLLGSGDYTHYKCDSPGMCGYDLYENDNAAWDYDNGIYSTQMYTQRVQQ
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLEAINNVTLA
LKTYGFYNNSSIIYSSDNGGQPTAGGSNWPLRGSKGTWEGGIRAVGVFVHSPLLKNKGTVCK
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVLDLHNIDPYTPRQKMAPG
QQAMSGTQLQSSQPSECTGNCLQEILATATGSPLSLSATWDRGTGGTMNGSPCQLAKVYGF
TSQPTHMRGWYLTGIQES

Important Features:

Signal Peptide:

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC
CCGTGCGGAGAATGCTCTGCCCCGGAGCCTTGCCTCCCGCTGCTGCTCTCTGGGTGBCAG
GTGGTTTCGGGAACGCGGCCAGTGC AAGGCATCACGGGTGTGTTAGCATCGGCACGTGAGCCT
GGGTCTGTCTACATATGGAACTAAACTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAAGTGCCTGGGACCAACAAAT
GCAGATGCTTTCCAGGATACACCGGAAAACTGCAGTCAAGATGTGAATGAGTGTGGAATG
AAACCCCGGCATGCCAACACAGATGTGTGAATACACCGGAAGCTACAAGTGTCTTTGCCT
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACCTTAGGACATGTGCCATGATAA
ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGA
CTCCGCCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAAAATGT CACA
TTGGTTTCGAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT
ATGGATAGCCATA CGTGCAGCCACCATGCCAATTGCTTCAATACCCAGGGGTCTTCAAGTG
TAAATGCAAGCAGGGATATAAAGCAATGGACTTCGGTGTTCTGCTATCCCTGAAAAATCTG
TGAAGGAAGTCTCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC
AAAAACAGCATGAAAAAGAAGGCCAAAAATTAAAAATGTTACCCAGAAACCCACCAGGACTCC
TACCCCTAAGGTGAACCTTGACGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAACCT
CTCATGGAGGTAAAAAAGGGGAATGAAGAGAAAAATGAAGAGGGGCTTGAGGATGAGAAAAGAG
AAGAGAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTCCCT
AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAGCGCTAACTTCCAA
ACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACT
GGAAACAGGATAGAGAAGATGATTTTGAAGCAGAACTCCTGCTGATCGAGATAATGCTATTGGC
TTCTATATGGCAGTTCCGGCCTTGCCAGGT CACAAGAAAGACATTTGGCCGATTGAACTTCT
CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGTCTCTTTGATTACCGGCTGGCCGGAG
ACAAAGTCCGGAAACCTTCGAGTGTGTTGTGAAAAACAGTAACATGCCCTGGCATGGGAGAAG
ACCACGAGTGGAGATGAAAAGTGGAAAGACAGGGAAAAATTCAAGTTGATCAAGGAACCTGATGC
TACCAAAGCATCATTTTTGAAGCAGAACTGCGGCAAGGGCAAACCGCGCAAAATCGCAGTGG
ATGGCCTCTGTCTGTTTTCAGGCTTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG
TTACTATCTTTATATTTGACTTTTGTATGTGCTGCTCCCTGGTTTGTGATATTGCATCATAG
GACCTCTGGCATTTTAGAATTACTAGCTGAAAAATTTGTAATGTACCAACAGAAAATATTATTG
TAAGATGCCTTCTTGATTAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT
TCTCAGTCAATTTCTGAATCTTTCCNCATTATATTATAAAATNTGGAANGTCAGTTTATCTC
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTTCTA
GAAAATAGAAAAAAGCACAGAGAAATGTTAACTGTTTGACTCTTATGATACTTCTTGGA
AATCATGACATCAAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC
TTGTATATTTAATTCTTTGTAATAATAA

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FIGURE 45

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCE
ATCEPGCKFGECVGPNNKCRCPGYTGKTCSDVNECGMKPRPCQHRVCVNTHGSYKCFCLSGH
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP
YNRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPTPK
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

Signal peptide:

amino acids 1-21

EGF-like domain cysteine pattern signature.

amino acids 80-91

Calcium-binding EGF-like domains

amino acids 103-124, 230-251 and 185-206

FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTGTCTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG
CGCTTCTCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCC
AGAATGGGAGCTGACTGATATGGTGGTGTGGGTGACTGGAGCCTCGAGTGGAAATTGGTGAGG
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTGTGCTGTGAGCCAGAAGAGTGCAT
GAGCTGGAAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAAGATATACT
TGTTTTGGCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGAATGTCCAGCGTTCTCTGTGC
ATGGATACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTG
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA
ATAGCATCCTGGGTATCATATCTGTACCTCTTCCATTGGATACTGTGCTAGCAAGCATGCT
CTCCGGGGTTTTTTTAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC
TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAGTCA
CAAAGACTATAGGCAATAATGGAGACCACTCCACAAGATGACAACCAAGTCTGTGTGCGG
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTGGATCTCAGAACAACTTTCTT
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAAAATC
TTTAAGACAAAACATGGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT
ACTTTTTAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAAATAATAAAG
ATTGCCATGAATCTTGCAAAA

CGCTGCTGCTGCTGTGGCTGCTGGTGTCTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG

FIGURE 47

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343
><subunit 1 of 1, 289 aa, 1 stop
><MW: 32268, pI: 9.21, NX(S/T): 0
M V V V V T G A S S G I G E E L A Y Q L S K L G V S L V L S A R R V H E L E R V K R R C L E N G N L K E K D I L V L P L D L
T D T G S H E A A T K A V L Q E F G R I D I L V N N G G M S Q R S L C M D T S L D V Y R K L I E L N Y L G T V S L T K C V L
P H M I E R K Q G K I V T V N S I L G I I S V P L S I G Y C A S K H A L R G F F N G L R L E T A T Y P G I I V S N I C P G P
V Q S N I V E N S L A G E V T K T I G N N G D Q S H K M T T S R C V R L M L I S M A N D L K E V W I S E Q P F L L V T Y L W
Q Y M P T W A W W I T N K M G K K R I E N F K S G V D A D S S Y F K I F K T K H D

Important Features:

Signal Peptide:

amino acids 1-31

Transmembrane domain:

amino acids 136-157

Tyrosine kinase phosphorylation site.

106-113 and 107-114

Homologous region to Short-chain alcohol dehydrogenase

amino acids 80-90, 131-168, 1-13. and 176-185

FIGURE 48

GCGACGTGGGCACCGCCATCAGCTGTTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGTTTC
 GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTGGG
 TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCCTCGGCACACGCTGGGCCCTCTGTCC
 TGATGCTGCTGAGCTCCTCGTGTCTCTCGCTGGTTCTGTCTACTTGGCCTGGATCCTGTTT
 TTCTGCTCTATGATTTCGTCAATTGTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT
 GTGGCTCAGTTTTCGGGAAGGTCCAAGAACCCAGGGCAAGGCTAAGAGGCACTGAGCCCTCA
 ACCCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCCTGTG
 GACAGCGTGGCCCCCGGCCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTTGGCGAGTGGCCC
 TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCACATCTGCAGCGGCTCCTTGGTGGCAGACAC
 CTGGGTCTCTACTGCTGCCCCTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCTCGGT
 CAGTGGTCTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG
 GCTGCCCTGCAGTTGCCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT
 GCAGCTCGCCCAACCCACGACCCACACACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCC
 CCTTTGGAGCCCTCTGCTGGGCCACTGGCTGGGATCAGGACACCACTGATGCTCCTGGGACC
 CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACATGTATCTACACCAGCT
 GCACCAGCGACACCTGTCCAACCCGCGCCCGCCTGGGATGCTATGTGGGGGCCCCAGCCTG
 GGGTGCAGGGCCCTGTCTCAGGAGATTCCGGGGCCCTGTGCTGTGCTCGAGCCTGACGGA
 CACTGGGTTTCAAGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGT
 GCTGCTGACCAACACAGCTGCTCACAGTTCTTGGCTGCAGGCTCGAGTTTCAAGGGGCGAGCTT
 TCCTTGGCCAGAGCCAGAGACCCCGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA
 TCCTTGAGGACAGCAGCTCCCAAGCAGGAGCACCCCTCCCATGCGCCTGGGAGGCCAGGCT
 GATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGCGGTGCTAACTG
 CTGCCCATGCTTTCATTGGGCGCCAGGCCCCAGAGGAATGAGCGTAGGGCTGGGGACCCAGA
 CCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCTGAGGGGGG
 CTACGACATGGCCCTCCTGCTGCTGGCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC
 TCTGCCTGCCCTATCTGACCACACCTGCGCTGATGGGGAGCGTGGCTGGGTTCTTGGGAGGG
 GCCGCCCCAGGAGCAGGCATCAGCTCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAG
 GGCTGACAGCCGCTGCTATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCGCGGGATGG
 TGTGTACCAAGTGTGTGGGTGAGCTGCCCAGCTGTGAGGGCCTGTCTGGGGCAACCATGGTGT
 CATGAGGTGAGGGGCACATGGTTCTTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAAGG
 CCCCGCCAGGCGCGGCTTTCACCGCGCTCCTGCTATGAGGACTGGGTGAGCAGTTTGG
 ACTGGCAGGTCTACTTCGCCGAGGAACAGAGCCCGAGGCTGAGCCTGGAAGCTGCTGGCC
 AACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC
 AGGCAGGCAAAATGGCATTACTGCCCTGTCTCCCCACCTGTCTGTTGTGATTCCAGGCAC
 CAGGGCAGGCCGAGAAGCCAGCAGCTGTGGGAAGGAACCTGTGGGGCCACAGGTGCCCA
 CTCCCCACCTGCAGGACAGGGGTGTCTGTGGACATCCCCACCCCACTGTCTACCAAGC
 AGGCGTCTCAGCTTTTCTCTCTCTTTACTCTTTTTCAGATCAATCAGCCAGCCAGTTTGT
 TGAATAATTTCTTTTTTTTGGGGGGCAGCAGTTTTCTTTTTTTTAACTTAAATAAATTTGTAC
 AAAATAAAA

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FIGURE 49

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571

MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV
PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGA
EEVGVAALQLPRAYNHYSQGSDDLALLQLAHPHTHTPLCLPQPAHRFPFGASCWATGWDQDTS
DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARFGMLCGGPQPGVQGPGCGDGGGPVLC
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEMSDEDS
CVACGSLRTAGPQAGAPSPWPWEARLMHQQLACGGALVSEEAVLTAHCFIGRQAPEEWSV
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLDPDGERG
WVLGRARPGAGISSLQTVPTLLGPRACSRHLHAAPGGDGSPI LPGMVCTSAVGELPSCEGLS
GAPLVHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEP
GSCLANISQPTSC

Important features:

Signal peptide:

amino acids 1-15

Homologous region to Serine proteases, trypsin family

amino acids 79-95, 343-359 and 237-247

N-glycosylation sites.

amino acids 37-40 and 564-567

Kringle domains

amino acids 79-96, 343-360 and 235-247

FIGURE 50

CGGGCCGCCCCCGGCCCCATTGCGGCCGGGCTCGCTGCGGCGGCGACTGAGCCAGGCTGG
GCCGCGTCCCTGAGTCCCAGAGTCGGCGCGGGCGGGCAGGGGCAGCCTTCCACCACGGGGAG
CCCAGCTGTCAGCCGCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGT
GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG
TCCCTGAAGACCCAGTGGTGGCACTGTGTGGGCACCGATGCCACCTGTGCTGCTCCTTCTCC
CCTGAGCCTGGCTTACGCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACA
GCTGGTGCACAGCTTTGTGTAGGGGCCAGGACACAGGGCAGCGCCTATGCCAACCGCACGGCCC
TCTTCCCAGACCTGTGTCAGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGCCTGTGGCG
GCAGAGGGCAGCTTCACTGTCTGTGAGCATCCGGGATTTCGGCAGCGCTGCCGTGAGCCT
GACAGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCCAACAGGACCTGCGGC
CAGGGGACACGGTGACCATCACGTGTCTCCAGTACCAGGGCTACCCCTGAGGCTGAGGTGTTT
TGGCAGGATGGGCAGGGTGTGCCCTGACTGGCAACGTGACCAAGTGCAGATGGCCAAACGA
GCAGGGCTTGTGTGTGTGCACAGCGCTCTGCGGGTGTGTCTGGGTGCGAATGGCACCTACA
GCTGCCTGGTGCACAAACCCGTGTGTGCAGCAGGATGCGCACRGCTCTGTACCATTACAGGG
CAGCCTATGACATTTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT
TGCACTGCTGGTGGCCCTGGCTTTCTGTGTCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG
AGAATGCAGGAGCTGAGGACACAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT
CTGAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGG
GAGCTGTACCCCTCCCTACAGCTCCTACCTCTGGCTGCAATGGGCTGCACTGTGAGCCC
TGCCCCAACAGATGCATCCTGTCTGTACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC
AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTTCCAAGTCATCCTGCTGCCTTTT
TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTTCTCTAAGTCATCCTGCCTGCT
GCCTTATTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCCTC
TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTTCTCCAAAAGATGCAATATTGAGA
CTGACTGACCCCTGCCTTATTTACCAAAGACACGATGCATAGTCAACCCGGCCTTGTTC
TCCAATGGCGTGATACACTAGTGATGTTGAGCCCTGCTTCCACCTGCATAGAATCTTT
TCTTCTCAGACAGGGACAGTGCGGCCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCTTTCT
CCCTCCTTCTCCTGCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG
AGGGGACTGCCCCCACCACCATGGTGTATTTCTGGGGCTGGGGCAGTCTTTTCTGGC
TTGCCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCTTCCG
GATGTCTCTCTCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC
TCGGAGGGATTTGTAACTGGGGTATATTTGGGGAAAATAAATGTCTTTGTAAAAAAA
AAAAAAAAAAAAA

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FIGURE 51

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386
><subunit 1 of 1, 316 aa, 1 stop, 1 unknown
><MW: -1, pI: 4.62, NX(S/T): 4
MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQ
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDQGQGVPL
TGNVTTSQMANEQGLFDVHVSFLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEENAGAEDQDGELEGSKTALQPLKHSDSKED
DGQEIA

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

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POST=0912/64

FIGURE 52

TTCTGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC
CTGAACCTTGCTCGAAGCCCTTGTCCGTAAGCCTTGAACCTACGTCTCTTAAATCTATGAAGTCG
AGGGACCTTTTCGTGCTTTTGTAGGGACTTCTTTCCCTTGCTTCAGCAACATGAGGCTTTTCT
TGTGGAACCGGGTCTGACTCTGTTTCGTCACTTCTTTGATTGGGGCTTTGATCCCTGAACCA
GAAATGAAAAATTGAAGTTCTCCAGAAGCCATTTCATCTGCCATCGCAAGACCAAGGAGGGGA
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAAGGACGGCTCCTTATTTCACTCCACTC
ACAAACATAACAATGGGTGAGCCCATTTGGTTTACCCTGGGCGATCCTGGAGGCTCTCAAAGT
TGGGACCAGGGCTTTGAAAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCAATTCCTCCTGC
TCTGGGCTATGAAAAAGAAGGAAAAGGTAAAATTCCTCCAGAAAGTACACTGATATTTAATA
TTGATCTCCTGGAGATTGAAATGGACCAAGATCCCATGAATCATTTCCAGAAATGGATCTT
AATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA
ACATGTTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTGATAAAG
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA
TAGAGATACATCTACCCTTTTAAATATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAA
AGAACATTTTATTTTATACAATGTTCTTTCTTGCTTTGTTTATTTTATATATATTTTT
CTGACTCCTATTTTAAAGAACCCTTAGGTTTCTAAGTACCCATTTCTTCTGATAAGTTATT
GGGAAGAAAAAGCTAATTTGGTCTTTGAATAGAAGACTTCTGGACAATTTTCACTTTCACAG
ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACC
ACGACATGAGACCAGGTTATAGCACAAATTAGCACCTATATTTCTGCTTCCCTCTATTTTCT
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT
GTTATAATGAAATAGTTTATGTGTAACGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA
TGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAAG
TTAGAACAAGGTTAATAGCCAGGCGATGGTGGCTCATGCTGTGTAATCCAGCACTTTGGGAG
GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA
CCCTATCTCTACTAAAAATACAAAGTAGCCCGGCGTGGTGTGCTGCTGTAATCCAGCT
ACCCAGGAAGGCTTGAGGCGGCAGAAATCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAG
ATCACCTNACGCTGGCACTCTGTCTCGAAAAAAGAAAAACACGGTTAATACCATATNA
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTTGGCTCCTAGTGAT
TGGTGGCCTATTATGATAAATAGGACAAATCATTTAAGTGTGAGTTTCTTTGTAATAAAATG
TATCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGC
TAGCGGAATATCCTTCTCGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA
TTGTATCATAAAGATAAAGTAGTAAACCAGTCTACATTTTCCATTCTGTCTCATCAAAAAC
TGAAGTTAGCTGGGTGTGGTGGCTCATGCTGTAATCCAGCACTTTGGGGGCCAAGGAGGG
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCCTCTA
CTAAAAATACAAAATTAGCCAGGCGTGGTGGTGGCAACCTGTAGTCCAGCTACTCGGGAG
GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGTCAGTGAGCCAGATTTGTGCC
ACTGCACTCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAGAAAGCAGAG
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATT

[illegible]

```
><subunit 1 of 1, 211 aa, 1 stop
```

MRLFLWNAVLTLFVTSLSIGALIPPEVEKIEVLQKPFICHRKTKGGDMLLVHYEGYLEKDGSL
 FHSTHKHNNQPIWFTLTGILEALKGWDQGLKGMCVGEKRKLIIPALGYGKEGKGKIPPEST
 LIFNIDLLERNGPRSHESFQEMDLNDDWKLKDEVKAYLKKEFEKHGAVVNESHHDALVED
 IFDKEDDKDGFISAREFTYKHDEI.

Signal peptide:

N-glycosylation site.

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

FIGURE 54

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTAGCAT
CCAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCCCTCTCCCGTAGCCCCACCGA
CTAACATCTCAGTCTCTGAAAATGACACAGAGATGCTGGCTACCTCGCCCTGCCCTCAGCCT
CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTACAGTAC
CTGCCACCTCAACGTCCTCAATGGCTCTGAGCGCCGCTGCCCTGCACCTTCAACTCCTGC
TACACAGTGAACCAAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTC
TGAGGAGATGTTCTCCAGTTCCCGCATGAAGATCATTAACTGAAGCTGGAGCGGTTTCAAG
ACCGCTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTCGGTGATGCTGAGAAACGTG
CAGCCGGAGGATGAGGGGATTACAACCTGCTACATCATGAACCCCTGACCGCCACCGTGG
CCATGGCAAGATCCATCTGCAGGTCCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG
CCGTGATTGTGGGTGCCCTCGTCGGGGGCTTCTGGCTGTGGTCACTCTGGTGCTGATGGTG
GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA
GGAGGGCAAGACGGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGTGGCCGGCC
CTGCAGCCTCCCGTGTCCCGTCTCCTCCCTCTCGCCCTGTACAGTGACCTGCCTGCTCG
CTCTTGGTGTGCTTCCCGTGACCTAGGACCCAGGGCCACCTGGGGGCTCCTGAACCCCG
ACTTCGTATCTCCACCCTGCACCAAGAGTGACCCAATCTCTTCCATCCGAGAAACCTGCCA
TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGGCTCCACCTGCCAGTCCCTGG
GGGGAGGCAGGAGGCACATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGA
GGAGGGGCGCTGTCACTGCCAGTGCTTGCTGGCAGTGGCTTACAGAGAGGACCTGGTGG
GGAGGGAGGGCTTCTGTGCTGACAGCGTCCCTCAGGAGGGCTTGGCCTGGCACGGCTG
TGCTCCTCCCCTGCTCCAGCCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCCTGA
AATTGGAGGGGCATGTTAAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAGCCAGGG
CTGCAGGCAAGCTGGACATGTGCCCTGGGCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT
GCTAGTGGCTCCTTGGGGCTCCTGTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG
ACTGGAAGAGCAGCTCCAGGTAGGGGCCATGTTTCCAGCGGGGACCCACCAACAGAGGCC
AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGTTGAATGCAGGTTGCTGCAG
GCTCTGCCTTCTCCATGGGGTAACCAACCTCGCTGGGCAGGGGCAGCCAAGGCTGGGAAAT
GAGGAGGCCATGCACAGGTGGGGCAGCTTCTTTGGGGCTTCACTGAGAATCTCCAGTT
GCCCTTGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGAAGGGAAAGCCTGAGGCCG
GCATAAGGGGAGGCCCTTGAACCTGAGCTGCCAATGCCAGCCCTGTCCCATCTGCGGCCACG
CTACTCGTCTCTCTCCAAACAACCTCCCTTCTGTTGGGACAAAAGTGACAATTGTAGGCCAGGC
ACAGTGGCTCACGCCCTGTAATCCAGCACTTTGGGAGGCCAAGGCGGGTGGAATTACCTCCAT
CTGTTTAGTAGAAATGGGCAAAACCCATCTCTACTAAAATACAAGAATTAGCTGGCGTG
GTGGCGTGTGCTGTAATCCAGCTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG
GGAAGCAGAGGTTGAGTGAACTGAGATGATGATGCTGCAATTCAGCCTGGGTGAC
ATAGAGAGACTCCATCTCAAAAAAA

FIGURE 55

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415
<subunit 1 of 1, 215 aa, 1 stop
<MW: 24326, pI: 6.32, NX(S/T): 4
MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNLVNGSDARLPCTFNSCYTVNHKQ
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRNVQPEDEGI
YNCYIMNPPDRHRGHGKIHLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRK
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

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FIGURE 56

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCCACCCNACTAACATCTCAGTCTCTGAA
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCCTTCAGCCTCACGGGGCTCAGTCTCTTTT
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC
TCAATGGCTCTGACGCCCCGCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC
AGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCTCCAG
TTCCGCATGAAGATCATTAACTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG
GAACCCAGCAAGTACGATGTGTGGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA
TTTACAACCTGCTACATCATGAACCCCCC

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FIGURE 57

TCACGGGGCTCATCTCTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTNCACATA
CCTGCCACCCCTCAACGTCCTCAATGGCTTTGACGCCCGCCTGCCCTGCACCTTCAACTCCNG
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTACCAGGAGTGCAACAACCTGGC
TCTGAGGAGATGTTCTCCAGTTCCCGCATGGAAGATCATTTAACTGAAAGCTGGAAGCGG
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAACCCAGCAAGTACGATGTGTGCGTGATGC
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTACAAC TGCTACATCATGAACCCCC

10501" 2218.651

FIGURE 58

TGCGGGGACCGTGGTACACCAATGGGCCCTCCACCTCCGCCCCCTACCGTGTGGGGCTGCTCCGGGATGGCCTCCTGT
 TCCTCTTGGTCTGCTGCTTAATGTCTGCTCGCGGACCCAGCGCTCCGCGCCGGAACGTCCACCCCACTGGTCTGGTCC
 CTGGTGAITTTGGGTAAACCACTGGAAGCCAAAGCTGGACAGCCGACAGTGGTGCATACCTCTGCTCCAGAAGA
 CGAAAGCTACTTCAACAATCTGGCTGAACCTGGAAGTCTGCTGCTGTATCATTTGACTGCTGGATTTGACAATA
 TCAGGCTGGTTTACAACAACAAATCCAGGGCCACCCAGTTTCTTGATGGTGTGGATGTACGTGTCCCTGGCTTTG
 GGAAGAGCTTTCTCCTGGAAGTTCTCGAGCCCGACGAAAGCAGCGTGGTTCCTATTTCCACACCATGGTGGAG
 GCCTTGTGGGCTGGGCTACACACGGGGTGAAGATGTCCGAGGGGCTCCTATGACTGGCGCGAGCCCCAAATG
 AAAACGGGCCCTACTTCTTGGCCCTCCGGAGATGATCGAGGAGATGTACCAGCTGTATGGGGGCCCGTGGTGC
 TGGTTGCCACAGTATGGGCAACATGTACACGCTCTACTTTCTGCAGCGGCAGCCGAGGCTTGAAGGACAAGT
 ATATCCGGGCTTCTGTCTACTGGGTGCGCCCTGGGGGGGCGTGGCCAGACCCCTGCGCGTCTCTGGCTTACAGGAG
 ACAACAACCGGATCCAGTCTATCGGGCCCTGAAGATCCGGGAGCAGCAGCGGTGAGCTGTCTCCAACGCTGGC
 TGCTGCCCTACAACATACATGGTCACTGAGAAGTGTTCGTGCAGACACCCAACTCACTACACACTCGGGG
 ACTACCGCAAGTCTTCCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGGCAGGACACAGAAGGGCTGGTGG
 AAGCCACGATGCCACCTGGCGTGCAGCTGCACTGCCTCTATGGTATGCGCGTCCCAACACAGACTCTCTTACT
 ATGAGAGCTTCCCTGACCGTGACCTAAATCTGCTTTGGTGACGGCGATGGTACTGTGAACCTGAAGAGTGCCC
 TGCAGTGCCAGGCTTGGCAGAGCCGCGAGGACCAAGTGTGCTGCAGGAGCTGCCAGGCGAGCAGCATCG
 AGATGCTGGCCAAACGCCACCCCTGGCCTATCTGAAACGTGTGCTCTTGGGCCCTGACTCTCTGTGCCACAGGA
 CTCTGTGGCTCGGCCGTGGACCTGCTGTGGCTCTGGGGCTGTCTATGGCCACGCGCTTTTGAAGAGTTGTGA
 CTCACCATTAAGGCCCGGAGTCTTGGACTGTGAAGCATCTGCCATGGGAAGTGTCTTTTGTATCTTTCTCT
 GTGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAGAAATGCTGCTGATGGTGA
 ACTGCTGTGACTTTAGGACTGGCTCCACAGGGTGGACTGGCTGGGCCCTGGTCCAGTCTCTGCTGGGGCCATG
 TGTCCCCCTATTCTGTGGGCTTTTATACTGTGCTACTGGGCCCTGGGCCCGCAGGCTTCTATGAGGGATGTT
 ACTGGGCTGTGGTCTGTACCCAGAGGTCCAGGGATCGGCTCGTGGGCCCTGGGGTGACCTTCCCAACACCA
 GCCACAGATAGGCTGCCACTGGTCTATGGGTAGCTAGAGCTGCTGGCTTCCCTGTGGCTTAGCTGGTGGCCAGCC
 TGACTGGCTTCTGGGCGAGCTTAGTAGCTCCTGCAGGCAGGGGAGTTTGTGTGCTTCTTCTGGTTTCCAGGC
 CCTGGGACATCTACTCCACTCTTACTCTCTTACCACAGGAGCATTCAGCTCTGGATGGGCGAGAGATGTG
 CCCCCAGTCCCGAGGCTGTGTTCCAGGGGCCCTGATTTCTCGGATGTGCTATTGGCCCCAGGACTGAAGCTGC
 CTCCCTTACCCCTGGGACTGTGGTTCCAGGATGAGAGCAGGGGTGAGGCCATGGCTTCTGGGAACCTATGGA
 GAAAGGGAATCCAGGAAGCAGCCAAAGCTGCTGCGAGCTTCCCTGAGCTGACCTTGTGTAACCCACCATCA
 CACTGCCACCTGCGCTAGGCTCTCACTAGTACCAAGTGGCTCAGCACAGGGCTGAGGATGGGGCTCTATCCAC
 CCTGGCCAGACCCCACTTTAGTCTGGGACTAGCCAGAACTGGAATGGGACCTGAGAGAGCCAGGGGTCCCC
 TGAAGGCCCTTAGGGCTTTCTGTCTGCCCCAGGGTGTCCATGATCTCTCTGGCGAGCAGGCATGGAGAGT
 CAGGGCTGCCCTTATGCGAGTAGGCTCTAAGTGGGTGACTGGCCACAGGCCGAGAAAGGGTACAGCCTCTAGGT
 GGGGTTCCAAAGAGCCCTTCAGGCTGGACTGAGCTGCTCTCCACAGGGTTTCTGTGACGCTGGATTTTCTGTG
 TTGCATACATGCTGGCATCTGTCTCCCTTGTTCCTGAGTGGCCCCACATGGGGCTCTGAGCAGGCTGTATCTG
 GATTCTGCAATAAAGTACTCTGGATGCTGTAAAAAAGAAAAAAAAAAAAAAAAA

09978158.101501

FIGURE 59

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189
><subunit 1 of 1, 412 aa, 1 stop
><MW: 46658, pI: 6.65, NX(S/T): 4
MGLHLRPYRVGLLPDGLLFLLLLLLMLLADPALPAGRHPVVLVPGDLGNQLEAKLDKPTVVH
YLCSSKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDRVVPFGKTFSL
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEMMQ
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRLVLASGDNNRI
PVIGPLKIREQQRSAVSTSWLLPYNYTWSPEKVVFVQTPTINYTLRDYRKFFQDIGFEDGWL
RQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCC
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLGPF

Important features:

Signal peptide:

amino acids 1-28

Potential lipid substrate binding site:

amino acids 147-164

N-glycosylation sites.

amino acids 99-102, 273-276, 289-292 and 398-401

Lipases, serine proteins

amino acids 189-201

Beta-transducin family Trp-Asp repeat

amino acids 353-365

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FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCGAGCGGCGGACGCGGCGACATGGAGAGCGGG
GCCTACGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTCGCGCGCTTCTCTGACGACGCGCA
GGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTG
AGGGGTACAGCAATGCCACGAGTCTAAGCAGATGTACTGCGTGTTC AACCGCAACGAGGAT
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGT
GGTCGACGCGTATTTCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTGTGGTTTCTGCTTCCTCACCAAC
CAGTGGGCAGTCACCAACCGAAGGACGTGCTGGTGGGGGCGGACTCTGTGAGGGCAGCCAT
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGACCCCCAACA
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCTTCACCCAGAA
CGCGGAGACCACCGAGGGCTACCAGCCGCCCTCTGTGTACTGAGTGGCGGTTAGCGTGGGAA
GGGGGACAGAGAGGGCCCTCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACCTGCCA
GCCCTCTCTTTACCTGTTCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC
TGGCGGGGGCTGGCAGAGCCACCCCCAAGTGCCTGTGCCAGAGGGCTTCAGTCAGCCGCT
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCTCGCTTTTAATGA
CCTCAGCCCCGCTGCGAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCCT
CAGCTTCCCCCGGCCCGGTGAGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG
ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGACACAGGCTCTGTGTCTCTCA
CTCAGGTTTGCTTCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCTGTGCCGCT
GGCCTCTGGGCTGCCCTCCCGTGGTGTGAGGCGGGGCTGGTGTCTATGGCACTTCTCTCTTG
CTCCACCCCTGGCAGCAGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTC
TGCAGTTGTTACTTAGGAAGCCTGGGAGGGCAGGGGTGCCCATGGCTCCAGACTCTGTCT
TGTGCCAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACG
GAATAAATGTTTCTCATTCAAAG

0970703-10501

FIGURE 61

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24810, pI: 4.75, NX(S/T): 1
MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEYSNAHESKQMYCVFN
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIIGDLLFSALWTFWLVGFC
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

Important features:

Type II Transmembrane domain:

amino acids 1-45

Other transmembrane domains:

amino acids 74-90, 108-126 and 145-161

N-glycosylation site.

amino acids 97-100

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TQSTN.8818/660

FIGURE 62

GAGCCACCTACCTGCTCGAGGCCAGGCCCTGCAGGGCCTCATCGGCCAGAGGGTGATCAGTGAGCAGAAGGATG
 CCCGTGGCCGAGGCCCCCGAGGTGGCTGGCGGCCAGGGGGACGGAGGTGATGGCGAGGAGCCGAGCCAGGGG
 ATGTTCAAGGCCCTGTGAGGACTCCAAGAGAAAAGCCCGGGGCTACTCTCGCCTGGTGGCCCTGTTGTGCTGCTG
 GCCCTGCTCGTGTGGCTTCGCGGGGGTCTACTCTGGTATTTCTTCAAGGTACAAGCGCGAGGTGATGGTCAGC
 CAGGTGTACTCAGGCAGTCTCGGTGTACTCAATCGCCACTTCTCCAGGATCTTACCCGCGGGGAATCTAGTGCC
 TTCGCACTGAAACCGCAAGCCCAAGAGATGCTCAGGAGCTCATCACCAGCACCCGCTCGGAACTTACTAC
 AACTCCAGCTCCGTCTATTCTCTTTGGGAGGAGACCCCTCACCCTGCTTCTCTGGTTCAATCTCCAAATCCCCGAG
 CACCGCCGCGTGTGCTGAGCCCGAGGTGGTGACGGCAGTCTGGTGGAGGAGCTGCTGTCCACAGTCAACAGC
 TCGCTGCGCTCCCTACAGGGCCGAGTACGAAGTGGACCCCGAGGGCTTAGTGATCTGGAAGCCAGTGTGAAA
 GACATAGCTGCAATTGAATTCACGCTGGGTGTGTACCGCTACAGCTACGTGGGCCAGGGCCAGGTCTCCGCGCT
 AAGGGCCCTGACCACTTGGCTTCAGCTGCTGTGGCACTGCAGGGCCCAAGGACCTCATGTCTCAAATCCCGG
 CTGGAGTGGACGCTGGCAGAGTGGCCGGAACGAGTGGCCATGTATGACGTGGGCGGGCCCTGGAGAAAGAGGCTC
 ATCACCTCGGTGTACGCTGCGAGCCGACAGGAGCCGTTGGTGGAGGTTCTGGCGCTCGGGGCCATCATGGCGGTC
 GTCTGGAAAGAGGCCCTGCACAGCTACTACGACCCCTTCGTGCTCTCCGTGACGCGGTGGTCTTCCAGGCCGT
 GAAGTGAACTTGACGCTGGACAACAGGCTCGACTCCAGGGGCTCCTCAGCACCCGCTACTTCCCCAGCTACTAC
 TCGCCCAAAACCACTGCTCCTGGCACCCTCAGGTCGCCCTCTCTGGACTACGGCTTGGCCCTCTGGTTTGTATGCC
 TATGCACTGAGGAGGCAGAGTATGATTTCGCGTGACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGT
 GGCTTGGCATCCTCGCAGCCCTACGCGAGAGGATGCCCGTGGTGGCCAGCGCGGATCAACATCAACTTACC
 TCCAGATCTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTGTACAACAGTCCGAGCCCTGCCCTGGA
 GAGTTCTCTGTTCTGTGAATGACTCTGTGTCCTGCTGTGATGGGGTCAAGGACTGCCCAACGGGCTGGAT
 GAGAGAACTGCGTTTGACAGGCCACATTCCAGTGCAAGAGGACAGCACATGCATCTCACTGCCCAAGGCTCTGT
 GATGGGCAGCCTGATTGTCTCAACGGCAGCGATGAAGAGCAGTGCAGGAGAGGGGTGCCATGTGGGACATTAACC
 TTTCCAGTGTGAGGACCGGAGCTGCGTGAAGAAGCCCAACCCGAGTGTGATGGGCGGGCCACTGTCAGGAGCGC
 TCGGATGAGGAGCACTGTGACTGTGGCTCCAGGGCCCTCAGCGCGATTTGTGGTGGAGCTGTGTCTCCCGAG
 GGTGATGGCCATGGCAGGCCAGCTCAGGTTTCGGGTGACACATCTGTGGGGGGGCCCTCATCGCTGCCACCG
 TGGGTGATAACAGCTGCCCATGCTCTCCAGGAGGACAGCATGCCCTCAGCGGTCTGTGGACCGTGTCTCCGGC
 AAGGTGTGGCAGAACTGCGCTGGCCTGGAGAGGTGTCTTCAAGGTGAGCGCGCTGTCTGATACCGGCTTACC
 GAAGAGGACGACCATGACTACAGCTGGCGCTGCTGCGAGCTCGACACCCGCTGGTGGCTCGGCGCGCTGCGC
 CCCGTGTGCTGCGCGCGGCTCCCACTTCTTCGAGCCCGGCTGCATCTGTGATTACGGGCTGGGGCGCCTTG
 CGCGAGGGCGGCCCATCAGCAACGCTCTGCAAAAGTGGATGTGCAAGTTGATCCACAGGACTGTGACGCGAG
 GCGATTCGCTACAGGTGACGCGACGATGTGTGTGCGGCTACCGCAAGGGCAGAGGATGGCTGTCAAGGT
 CATCAGGTGGTCCGTGGTGTGCAAGGCACTCAGTGGCGCTGGTTCTGCGGGGCTGGTCAGCTGGGGCCCTG
 GGCTGTGGCGGCTCAACTACTTCGGCGCTACACCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT
 ACCTGAGGAACTGCCCCCTGCAAGCAGGCGCCACCTCCTGGACTCAGAGAGCCAGGGCAACTGCCAAGCAGG
 GGGACAAGTATTCTGCGGGGGTGGGGAGAGAGCAGGCCCTGTGGTGGCAGGAGGTGGCATCTTGTCTGCTCC
 CTGATGTCTGCTCCAGTGTATGGCAGGAGGATGGAGAAGTGCCAGCAGCTGGGGGTCAAGACGCTCCCTGAGGACC
 CAGGCCCCACCCAGCCCTTCTGCTCCCAATCTCTCTCTCTCGTCCCTTCTCTCACTGCTGCTAATGCAAG
 GCAGTGGCTCAGCAGCAAGAAATGCTGTTTACATCCGAGGAGTGTCTGAGGTGCGCCCCACTCTGTGACAGAG
 CTGTTTGGCGAGCCTTGGCTCCAGAGAGCAGATTCCAGCTTCGGAAGCCCTGGTCTAAGCTTGGGATCTGGGAAT
 GGAAGGTGCTCCATCGAGGGGGACCTCAGAGCCCTGGAGACTGCCAGGTGGGCCCTGCTGCCACTGTAAAGCCAA
 AAGGTGGGAGTCTCTGACTCCAGGGTCTTGGCCACCCCTGCTGCCACTGGGCGCTCAGCGCCAGCAGCCCT
 CACTGGAGGTGAGCTCAGCTGCCCTTGGAAATAAAGCTGCTGATCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152
><subunit 1 of 1, 802 aa, 1 stop
><MW: 88846, pI: 6.41, NX(S/T): 7
MPVAEAPQVAGGQDGGDGEEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL
LWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT
YNNSSSVYSFGEGPLTCFFWFILQIPEHRRMLSPVVQALLVEELLSTVNSSAAVPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGVRLRKGPDLHASSCLWHLQGPDKDML
KLRLWTLAECDRLAMYDVAGPLEKRLITSVYGC SRQEPVVEVLASGAIMAVVWKGLHSY
YDPFVLSVQPVVFQACEVNLTLNRLDSQGVLSPTYFPSPYSPQTHCSWHLTVPSLDYGLAL
WFDAYALRRQKYDLPCTQGQWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP
GVRVHYGLYNQSDPCPGEFLCSVNGLCVPACDGVKDCPNGLDERNCVCVRATFQCKEDSTCIS
LPKVCDDGQPDCLNGSDEEQCQEGVPCGTFTFQCEDRSCVKKPNPQCDGRPDGRDGSDEEHCD
CGLQGFPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIAADRVITAACHCQEDSMAS TVL
WTVFLGKVVQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPA
RSHFPEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSBAYRYQVTPRMLCAGYRKG
KKDACQGDSSGGLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIIQVVVT

Important features:

Type II transmembrane domain:

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447
and 509-512

Kringle domains.

amino acids 746-758 and 592-609

Homologous region to Kallikrein Light Chain:

amino acids 568-779

Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

FIGURE 64

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCAGAT
CTCCCTCACCGGCCCGGTGTGCGGGTGCACTATGGCTTGTACAACCAAGTTCGGACCCCTGCC
CTGGAGAGTTCCTCTGTTCTGTGAATGGACTCTGTGTCCCTGCTGTGATGGGGTCAAGGAC
TGCCCCAACGGCTGGATGAGAGAAACTGCGTTTGAGAGGCCAATTCCAGTGCAGAGAGGA
CAGCATATGCATCTCACTGCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTCACTTCCAGTGTGAGGACCGG
AGCTGCGTGAAGAAGCCCAACCCGAGTGTGATGGGCGGGCCGACTGCAGGGACGGCTCGGA
TGAGGAGCACTGTGACTGTGGCTCCAGGGCCCTCCAGCCGATGTTGGTGGAGCTGTGT
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTCGGGGTCGACACATCTGTGGG
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT
GGCCTCCACGGTGCTGTGGACCGTGTTCCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG
GAGAGGTGTCTTCAAGGTGAGCCGCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT
GACTACGACGTGGCGCTGTCTGCAGCTCGACCACCGGTGGTGCCTCGGCCCGCTGCGCCC
CGTCTGCCCTGCCCGCGCTCCCACTTCTTCGAGCCCGGCCTGCATTGCTGGATTACGGGCT
GGGGCGCCTTGCGCGAGGGCGGCCCATCAGCAACGCTCTGCAGAAAGTGATGTGCAGTTG
ATCCACAGGACCTGTGCAGCGAGGCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC
CGGTACCGCAAGGGCAAGAAGGATGCCTGTGAGGGTGACTCAGGTGGTCCGCTGGTGTGCA
AGGCACTCAGTGGCCGCTGGTTCTGCGGGGCTGGTCACTGGGGCTGGGCTGTGGCCGG
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT
GACCTGAGGAACTGCCCCCTGCAAAGCAGGGCCACCTCCTGGACTCAGAGAGCCAGGGC
AACTGCCAAGCAGGGGGACAAGTAT

09978188-101501

FIGURE 65

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG
CTCCGTGCGGCCAAGTTTTCATTTTCCACCTTCTCTGCTCCAGTCCCCCAGCCCCCTGGCCG
AGAGAAGGGTCTTACCGGCCGGGATTGCTGGAAACACCAAGAGTGGTTTTTGGTTTTTAAA
ACTTCTGTTTCTTGGGAGGGGGTGTGGCGGGGAGGATGAGCAACTCCGTTCTCTGCTCTG
TTTCTGGAGCCTCTGCTATTGCTTTTGCTGCGGGGAGCCCGTACCTTTTGGTCCAGAGGGAC
GGCTGGAAGATAAGTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG
TTTAACCTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTTCGCCACAG
CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAACTTTTTTCATCATTCACGGAT
GGACGATGAGCGGTATCTTTGAAAACCTGGCTGCACAACTCGTGTGAGCCCTGCACACAAGA
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCACCAGCTTTACACGGA
TGCGGTCAATAATACCAGGGTGGTGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG
AGAAGGACGATTTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGACGTC
GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGATCCTTG
CGGGCCCATGTTTGAAGGGGCGACATCCACAAGAGGCTCTCTCGGACGATGCAGATTTTG
TGGATGTCCTCCACACCTACACGCTTCTCTCGGCTTGAGCATTGGTATTGAGATGCCTGTG
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGT
CTTGCGATCAATGTCATATGGAACAATCACAGAGGTGGTAAATGTGAGCATGAGCGAGCCG
TCCACCTCTTTGTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTTGCCTTCCAGTGCACT
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGAAGAACCGTTGTAATAGCAT
TGGCTACAATGCCAAGAAAATGAGGAACAAGGGAACAGCAAAATGTACCTAAAAACCCGGG
CAGGCATGCCTTTTCAGAGGTAACCTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA
CCTCCTTCTTAATACCATGCTGACAGAGCAGGGCACATCCTAGCCCAGGAGAAGTGGCCAGCA
CAATCCAATCAAATCGTTGCAAATCAGATTACACTGTGTCATGTCCTAGGAAAGGGAATCTTT
ACAAAAATAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

0078138.10501

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646
><subunit 1 of 1, 354 aa, 1 stop
><MW: 39362, pI: 8.35, NX(S/T): 2
MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRTSKDPEHE
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHLKLVSAHHTREKDANVVVDWL
PLAHQLYTDVNNTRVVGHISIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV
GRITGLDPAGPMFEGADIIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSLVDKPSFAFQCTDSNRFKKGICLS
CRKNRNCNSIGYNACKMRNKRNSKMYLKTRAGMPFRGNLQSLCEP

Important features:

Signal peptide:

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

FIGURE 67

CGGACGCGTGGGCGGACGCGTGGGCTTGGGCAAGGGCCGGGGCGCCGGGGCGAGCCACCTCTTCCCTCCCCCGC
 TTCCCTGTGCGCTCCGCTGCTGCTTGGAGCGCTGTGGAGGAGTGGAGCAGCACCCCGGCGGCCCTGGGGGTGACAGT
 CGGCAAGTTTGGCCGAAGAGGAAGTGGTCTCAAACCCCGGCGAGTGGCGACGAGCCAGGCGCGCTCG
 CTGCTTGGCGGGCGGGCTGTAGCGCAGGGCGCGCCCAGTGGCCGAGACCCGGGGCTCTCAGGAGCGCGCCCGGAG
 AGAAGAGTGGCGGGCGGACGAGAGAAACAATCTCAAAGTTTGGCGAAAGGACCGCCCTCTACTCCGGGGTGTGCG
 CCGCTCCCGCGCCCGAGCCCTGGCATCCAGAGTACGGGTGAGCGCCGGGCGATGGAGCCCCCTGGGAGGCGG
 CACCAGGGAGCTTGGGCGCCCGGGGCTCGCGCGCAGCCCATCGGGTAGACCCAGCAAGCTTCGGGACCCCTTCG
 GCACCTCTGGACCGCCAGGATGCTGTGGCCACCTCTCTCTCTCTCTCTGGAGGCGCTCTGGCCCATCCAG
 ACCGGATTATTTTCAAATCATGCTTGTGAGGACCCCCAGCAGTGTCTTAGAAGTGCAGGGCACTTTACAGA
 GGCCCTGTGTCGGGACGAGCCGACCTCTCCCTGGCACTGCACCTGGCTCATCTGGGACGAGGAAACAGACTG
 TCACCATCAGTGTCCAGAAGCTACACTGGCCTTGGGCTCAGAGCGCTTAAACCTACGCTCCCTCTCCAGCCAC
 TGATCTCTCTGTGTGAGGCACTCTCCAGCCCTCTGACGCTGGCCGGGGCAACGTCAACATCACTTACAGCTATG
 CTGGGGCCAGAGCACCCATGGGCGAGGGCTTCTGCTCTCTACAGCCAAGATTGGCTGATGTGCGCTGCAGGAAG
 AGTTTCAGTGCTGAACACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCTGTGGCGATGGCT
 CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGCTCCCTCCCTGGCTTGAATG
 TCACCTTGGAGGACTTCTATGGGGTCTTCTCTCTCTCTGGATATACACACCTAGCCTCAGTCTCCACCCCCAGT
 CCGCCATTGGCTGTGGACCCCCATGATGGCCGGCGGCTGGCCGTGCGCTTACAGCCCTGGACTTGGGGCTTTG
 GAGATGCAGTGATGTATGACGGCCCTGGGCCCTTGAGAGCTCCCGACTACTGCTAGTCTACACCCACTTCA
 GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTGTGTCTTACCACACAGTTGCTTGGAGCA
 ATGGTCTGGCTCTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGGCTTGGGACAGACCTGTGGCTTAGGCT
 CTGGCCTGGGAGCTGGCGAAGGCTTAGGTGAGCGCTGTCTACAGTGAGGACACGCTGTGACGCTCATGGGACT
 GTGCTGACGGCAGAGTAGAGGAGCTGCCAGGCTGCCACCTGGACACTTCCCTTGGGGCTGTGGCACT
 CTGGTGCCACAGCTCTGCTCCTGCTGTGACCGCTGCAACTACGAGACTTCTGTGCTGATGGAGCAGATGAGA
 GACGCTGTGCGATTGCGAGCTGGCAATTTCCGATGCGGGGACGAGAGTGTGCTGATGAGACGTGGGTGTGCG
 ATGGGACGCCAGCTGTGCGGACGGCGAGTGTGAGTGGGACTGCTCTATGTTCTGCCCCGACAGTCTATTACAG
 CTGCACTTATGGCAGCTAGTGTGCGGCTGCTCTGGTCTATGCGCCCTGGGCTGCACCTTCAAGCTCATAGCA
 TTGCAACCCCGGCTCTGGGCTTGTGCGGCTTGTGCCCCCTCTCCGGATGGAGGCTGAGATTGTGACGAGCAGGCA
 CCCCCCTTCTACGGGAGCTCATTTGCCAGGGTGCCATCCACCTGTAGAAGACTTTTACCGCAGGATGATGACT
 CCAGGAGGTGGCCAGGCTTCTGCTACAGATCTTACCGCAGGATGATGACTCCAGGAGGTGGCCAGGTTAATGATA
 AACTCAGTGTGGGCACTGTGCTAGCAGCTTCCAGCTTCCAGCTTCAAGCTTCTGCTGTCCCTTGGAGCCCTAGATG
 CCGCGCTGTGTCAGCGGGGCGCTTGTATGCCAGCGCTGGTACCGCTCTCCGCGCTGGGGCTGTCTCCCTCGAA
 CCAACACCCCGGCTCTGGGCTTGTAGCCAGATCCCAAGTCAACCTTCTGCTGTCCCTTGGAGCCCTAGATG
 GTGGCAGCTCTCAGCCCGTGTAGGGCGGGCAGTGGGTGAGGAGTGGGGCAGGACACCCCACTGCCATCA
 AGGCTCAGCTCCCATCTGCTAGCAGCTTCCAGCCCACTACTGTCTCTGAGGCCCCAGGGCCACTGCCCTCAC
 TGGCCCTAGAGCCATCATATTGTGTGAGTGGTGGAGGCCCTGGAGGGCCCGCTGTGTGGCCAGCTTGGGCCCC
 CAGGACCAACCCCGAGGCCCTTGGACCCACACAGCAGTCTTGGCCCTGGAAGATGAGGACGATGTGCTACTGG
 TGCACCTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGACAGAGGATGAGCCACTGCTTACCTGAGGGGAGTGGGG
 CTTACTAGGAGCTCTCCCTGGGGGCTCTACTCATAGTGGCAACCTTTTAGAGGTGGGTGAGCCTCCCTCC
 ACCACTTCTCTCCGTGCGGTGATTTCAGGGACTTGGTGGGCTCTCCGTGAGCCCTTAGAGCTGATATAAAGT
 TAAGTGTCTCAGGCGAGGAGGCTCAGAGTCTCTCTGTACGTGGGCAATGGCCAGACACCCAGTCCCT
 TCACCAACCTCTCTCCCAAGCCACCAATTTGGGTGGCTGTTTTAAAGTAAGATTTCTAGAGGATACATA
 GGTCTGGAACCTCTCTTCCAAACCTTACCCAAAGTGGCTTAAGCAACCGGAATGCCAATTAACATAGAGA
 CCTCCAGCCCAAGGGGAGGATTTGGGACAGACCTGAGGTTTTGCCATGCCAACAATCCTCTACAGGGCTGG
 CTCACAAAAGAGTGCACAAATGCTTCTATTCCATAGCTACGCGATTGCTCAGTAAGTTGAGGTCAAAAATAA
 GGAATCATACATCTC

09970368.101501.28102660

FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHFPDRIIFPNHACEDPPPAVLLEVGTLQRPLVRDSRTSPANCTWLIL
GSKEQTVTIRFQKLHLACGSERLTLRSPLOPLISLCEAPPSPLOLPGGNVTITYSYAGARAP
MQQGFLSYSQDWLMCLQEEFQCLNHRCVSAVQRCDGVDACGDGSDGSCSSDPFPGLTPRP
VPSLPCNVLTLEDFYGVFSSPGYTHLASVSHPPQSCHWLLDPHDGRRLLAVRFTALDLGFGDAVH
VYDGGPPPESSRLLRLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLP
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSWD CADGTDEEDCPGCPPGHFPCGAAGTSGAT
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRCDKCVYETWVCDGQPD CADGSDEWDSCS
YVLPRKVITA AVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEABIVQQQAPPSY
GQLIAQGAIPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQGRLMRRLVR
RLRRWGLLERTNTPARASEARSQVTPSAAPLEALDGGTGFPAREGGAVGGQDGEQAPFLPIKA
PLPSASTSPAPTTVPEAPGPLSPLEPSLLSGVVQALRGRLLP SLGPPGPTRSPPGPHTAV
LAL EDDDLVPLAEPGVWVARAEDEPLLT

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

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105101.238/660

FIGURE 69

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA
GACGCGATGGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGG
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC
AAGCCCCGAACCATATATTGTTATCACTGGATTGAAGTCACCGTTATCTTATTTTTCATA
CTTTTATATGTACTCAGACTTGATCGATTAAATGAAGTGTTATTTTGGCCTTGTCTTGATAT
TATCAACTCACTGGTAACAACAGTATTTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAA
GCCTGTGCATGAAAAAAAAGAAGTTTGTTAATTTTATATTACTTTTTAGTTTGATACTAAGT
ATTAAACATATTTCTGTATTCTTCCAAAAAAAAAAAAAAAAAAAA

10501-223269

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645
><subunit 1 of 1, 152 aa, 1 stop
><MW: 17170, pI: 9.62, NX(S/T): 1
MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTEFFIIAQAPEPYIVITGFVETVILFFILL
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTTLVGGGVFALVTAVCCCLAD
GALIYRKLLFNPSGPYQKKPVHEKKEVL

Important features:

Potential type II transmembrane domain:

amino acids 26-42

Other potential transmembrane domain:

amino acids 44-65, 81-101 and 109-129

Leucine zipper pattern

amino acids 78-99 and 85-106

N-myristoylation site.

amino acids 110-115

Ribonucleotide reductase large subunit protein

amino acids 116-127

FIGURE 71

GGGCGAGAAGTAGGGGAGGGCGTGTCCGCCGCGGTGGCGGTGCTATCGTTTTGCAGAACCT
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA
TGGATAACGTGCAGCCGAAAAATAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAAGCCCC
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATACTTTTAT
ATGTACTCAGACTTGATCGATTAAATGAAGTGTTATTTTGGCCTTGCTTGATATTATCAAC
TCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTNTTGCCGAC

FIGURE 72

CAGCCCCGCGCGCCGGCCGAGTGCCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG
CTGGGCGCGCCCCCGGGGCCCGCCGCTGGGGCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGC
CTCTGCTGGCCCCAGTGGCTCCTGCGCGCCGCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTG
CCCTCCGGGTGGCCGCGGCCACGAACCGGTAGTTGCGCCACCCCGGGACCCGGGACCCC
TGCCGAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCTGCCCTGGCGTCCCCCGCGG
GCGCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG
TAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT
CTAGCACATACCGCTCCAAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACG
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAA
CATTGCCACTATTTTGAATCAGAGAATTTCTTTTGGCTGGGATTAAATGGAATGGAATAC
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTCTCTGGAGACCTTCTTCGACTCC
CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCGCGTTGGC
CGTGTCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGTGGAATTGAACCAAGTTTGT
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTG
AAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC
CATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGG
AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGTTTCTGGACTGGGTCCAG
CTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAATCTCCATCTACCT
GAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCTCAGCTTTACATTACAGC
CCATGATGGGGGCGGCTGAATTATGAATGTTACCGATTGGGCATTTCCCCATCCACAAAT
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCAGAA
GAGGTGGGCTTCGACAGCGAGCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT
CCGGGCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCTCAGTCTTTGAGCGAG
CCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTT
AATCGTCTGCTGCTGCGGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTGCTCA
ATGATGAGTCCTCTCTGGTCAGACATCGCTGGAATGAATAGCCAGGCCTGACCTCAAGCAA
CCATGAACTCAGCTATTAAGAAAATCACATTTCAGGGCAGCAGCCGGATCGATGGTGGCG
CTTTCTCTGTGCCCACCCGCTCTTCAATCTCTGTTCTGCTCCAGATGCCTTCTAGATTAC
TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA
AAAAAAACTTCATTCTAA

FIGURE 73

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493

><subunit 1 of 1, 518 aa, 1 stop

><MW: 56180, pI: 5.08, NX(S/T): 2

MGALARALLLPILAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGLAL
ALEPALASPAGAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS
YIDTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESNF
FLPGIKWNGILGLAYATLAKPSSSLETFFDLSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS
LVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTLLR
LPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISYLRDENSRSFR
ITILPQLYIQPMMGAGLNYECYRFGISPSSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA
ETAGAAVSEISGPFSTEDVASNCVPAQSLSEPIWIVSYALMSVCAGAILLVLLVLLLPFR
QRRPRDPEVVNDESSLVRHRWK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

09978132 10501
TOSTOT" 88187660

FIGURE 74

CGCCTCCGCCTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG
GCAGCCGCCTGGCGGCGATCCAGGGCGGTGCGGGGCCCTGGGCGGAGCCGGAGGCGCGGCC
GGCATGGAGGCGCTGCTGCTGGGCGCGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA
CAACCTGGTGAAGGCCCGCCCGTGCGGCGGCATGGGCAACCTGCGGGGCCGACGGCCGTGG
TCACGGGCGCCAAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGAGCG
CGCGTGGTGTGGCCTGCCGAGCCAGGAGCGCGGGAGGCGGCTGCCTTCGACCTCCGCCA
GGAGAGTGGGAACAATGAGGTCACTTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC
GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCCTCATCCACAATGCC
GGTATCAGTTCCTGTGGCCGACCCGTGAGGCGTTTAACTGCTGCTTCGGGTGAACCATAT
CGTCCCTTTCTGCTGACACATCTGCTGCTGCCTTGCCCTGAAGGCATGTGCCCTAGCCCGG
TGGTGGTGGTAGCCTCAGCTGCCCACTGTGCGGGACGTCTTGACTTCAAACGCTGGACCGC
CCAGTGGTGGGCTGGCGGAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT
GTTTGCCCGGAGCTCGCCAAACAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCACC
CAGGGCCTGTGAACCTCGAGAGCTGTTCTGCGCCATGTTCTGGATGGCTGCGGCCACTTTTG
CGCCCATTTGGCTTGGCTGGTGTCTCCGGGCACCAAGAGGGGTGCCAGACACCCCTGTATTG
TGCTCTACAAGAGGGCATCGAGCCCTCAGTGGGAGATATTTTGCCAACCTGCCATGTGGAAG
AGGTGCCTCCAGCTGCCCAGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG
CTGGCAGGGCTTGGGCTGGGGAGGATGCTGAACCCGATGAAGACCCCACTGTGAGGACTC
AGAGGCCCATCTTCTCTAAGCACCCCCACCTGAGGAGCCACAGTTTCTCAACCTTACC
CCAGCCCTCAGAGCTCACCAGATTGTCTAAGATGACGCACCGAATTCAGGCTAAAGTTGAG
CCTGAGATCCAGCTCTCCTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCCTT
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGGTTGAAGGAAT
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT
AGACACTGTGCTTCTCGGAAATTGGATGTAGTATTTTCAGGCCCCACCCTTATTGATTCTG
ATCAGCTCTGAGCAGAGGCAGGGAGTTTGAATGTGATGCACTGCCAACATTGAGAATTAG
TGAACCTGATCCCTTTGCAACCGCTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCG
GAATTAGGCTCCCCAGACTAAGGACTCGCCTAGGGTCTCAGTGAAGTAGGAGGAGGGCCTG
GGATCTGAACCAAGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCATGGGAGTAAGGGGACGCTTCCGGGCGG
ATGCAAGGCTGGGCTCATCTGTATCTGAAGCCCTCGGAATAAAGCGGTTGACCGCCAAAA
AAAAAAAAAAAAAAAAA

FIGURE 75

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227
<subunit 1 of 1, 377 aa, 1 stop
<MW: 40849, pI: 7.98, NX(S/T): 0
MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGRTAVVTGANSIGIGKMTALELARRGAR
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG
ISSCGRTREAFNLLLRVNHIGPFLLTHLLLPCLKACAPSRVVVVASAAHCRGRDLDFKRLDRP
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHPGPVNSELFRLRHVPGWLRPLLR
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDRAAHLWEASKRL
AGLGPGEAEPEDEDPQSEDEAPSSLSTPHPEEPTVSQPYPSQSSPDLSKMTHRIQAKVEP
EIQLS

Important features:

Signal peptide:

amino acids 1-16

Glycosaminoglycan attachment site.

amino acids 46-49

Short-chain alcohol dehydrogenase family

amino acids 37-49 and 114-124

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INST. 0818/60

FIGURE 76

GGAGGAGACAGCCCTCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATGAGGAGCATGGCTCAG
 GACTCCCCGCCCCAGATCTTAGTTCACCCCCAGGACAGCTGTTCACGGGCCCTGGCCCTGCCAGGATGAGCTGC
 CAAGCCTCAGGCCAGCCAGCTCCCAACCATCCGCTGGTTGCTGAATGGGACGCCCTGAGCACTGGTGCCCCAGAC
 CCACACCACTCCTGCTGCTGATGGGACCTCTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCACGAGTGGCCAG
 GCCCTGTCCACAGACCTTGGGTGCTCTACACATGTGAGGCCAGCAACCCGGCTTGGCACGGCAGCTGACAGAGGCCGT
 GCGCTGTCTGTGGCTGTCTCTCGGGAGGATTTCCAGATCCAGCCTCGGGACATGTTGGCTGTGGTGGGTGAGCAG
 TTTACTCTGGAATGTGGGCCGCTTGGGGCCACCCAGAGCCCAAGTCTCATGTGGGAAAGATGGGAAACCCCTTG
 GCCCTCCAGCCCGGAAGGCCACAGGTGTCCGGGGGCTCCCTGTGATGGCAAGACAGAGAGAGTGTACAGAGGG
 ACCTACATCTGTGTGGCCACCAACGCGCAGGACATAGGGAGAGCCGCGAGCCCGGGTTTCATCCAGGAGGCC
 CAGGACATCAGCGAGCTGTGGAGCTCTGGCTGTGCGAATTCACTGGAAATGTGACACTGCTGAACCCGGAT
 CCTGACAGAGGCCCAAGCCTAGACCCGCGTGTGGCTCAGCTGGAAGGTCACTGGCCCTGCTGGCCCTGCCCAA
 TCTTACACGGCTTGTTCAGGACCCAGATGCCCGCGGAGGCCAGGGAGCTCCGTGGGCAGAGGAGCTGTGGCC
 GGTGGCAGAGCGCAGAGCTTGGAGGCCCTCCACTGGGCCAAGACTACAGATTCAAAGTGAGACCATCCTCTGGC
 CGGGCTCAGAGGCCCTGACAGCAACGTCTGCTCTGAGGCTGCCGGAAGAGTGGCCAGTCCCCACCTCAGGAA
 GTGACTCTAAGACCTGGCAATGGCAGTCTTGTGAGCTGGGTCCCAACCACTGCTGAAACCAACAATGGCATC
 ATCCGTGGCTACAGGCTTGGAGCTCTGGGCAACACATCACTGCCACAGCCAACTGGAGCTGTAGTTGGTGGAGCAG
 ACCGAGTGGAAATGCCACCCATAGCCAGGCTCCTACTGCGTGCAGTGGCTCAGTCACTGGTGGTGGAGCT
 GGGGAGCCCACTAGACCTGTCTGGCTCCTTTTAGAGCAGGCCATGGAGCAGGCCACCCAGAACCCAGTGTGAGCATC
 GTGCTTGGACCTTGGAGCAGCTGAGGGCTACCTTGAAGCGGCTGTAGGTTATGTGACACTTGGGCTGTTCAGCTC
 TGGCTGCTGCTTCTGGGACCCGCGGTGTGTATCCACCGCGCGCCGAGCTAGGGTGCACCTGGGCGCAGGTCTG
 TACAGATATACAGTGGAGATGCACTCTTAAACACAGGATGGATCACTGACTTCCAGTGGCTGGGCGCGATGCCCG
 TGGCGTTCCACCTCTGGCTCTCGGACCTGAGCAGCAGCAGCAGCTCAGCAGTGGCTGGGCGCGGATGCCCGG
 GACCCACTAGACTGTGCTGCTCTCTGCTCTCTGGGACTCCCGAAGCCCGCGGCTGCGCCCTGCTTCCAGACCC
 AGCACTTTTATGGCTCCCTCATGCTGAGCTGCCCTCCAGTACCCAGCCAGCCAAAGTCCCCAGCTCCAGCT
 GTCAGGCGCTCCACCCAGCTGGCCAGCTCTCCAGCCCTGTTCCAGCTCAGACAGCTCTGACGCGCCAGG
 GGACTCTCTTCTCCCGCTTGTCTTGGCCCTGACAGGCTTGAAGGCCAAAGAGACAGGAGCTGACGATC
 GCCAACAGTCCCCACTGCTCCGCGCCAGCCACTCTTGGAGCTCCGGGCTGTGAGTAGGAAATAGAGTTCC
 AAGAACCTTTCCAAAGCCCGAGGAGCTGTGCCCAAGCTCTGGTGTCTGGCGGCCCTGGGACCGAAATCTCTC
 AGCTCTCAATAGAGCTGGTTATCTGCTATCTCCCTCAGCACCCCTTCTTCATGAACTCCCCCACTCAG
 AGTCAACAGACCCAGCCTCCGGTGGCCACACAGGCTCCCTCTCCATCTTGTGTCGAGCAGCCCACTCCCATC
 CTTAGCCCTGACGTCCCCCTTCCGCCCCAGGCTCTTCCCTCTGAGGCTCCAGCAGCCCACTCCCTCTGCTG
 AGCTCTCTCACTGTCTCCCTGGGGAGGATCAAGACAGCGTCTCTCCATGCCAAGGGCTCCTTCAACCCCCACCACTAT
 CTTAGTGGGTGAGGAGTCCACGAAACAGCGTCTCACGGACATGGGACGAGCTGGAGGAGGGGTGGGGCCAGAGGG
 GGGTACATCAGCCTCCCAACAGCCTCAGAGTTTACGGACATGGGACAGGCTTGTGACGCTCTTCTCTGCTGAT
 GCTCACTTGTGTGCCCACTGGCAGTGGCTGTGGATAGCTTGTGTTTGGTCTGAGTCTTCCAGTCCCTCTCTGCTGAT
 TCAAGCTCTGAGGACAAATGGCGCCAGCGCAGGACAGGCTTGTGACGCTCTTCCAGTCCCTCTCTGCTGAT
 GTCCTCTATAGATGCTCATCACTTCCCTCCCGGGATGAGATCTTCTGACCCCAAGCTCTCCCTGCTGAT
 TGGAGTGGAGGCGCAGATGTGTTGAAGACATGGAGGTGAGCCACACCCAGCGCTGGGAAGGGGGATGCTCCC
 TGGCCCCCTGACTCTCAGATCTCTTCCAGAGAAGTCACTGCTGCTGATGCCAAGGCTGGTGTCTTCTCT
 GTAGATTACTCTGAACAGTGTCTCTGAGACTTCCAGAGCGGAAATCAGAACCACTTCTCTGTCCACCAAG
 ACCCTGGGCTGTGTGTGGTGTGTGGCTGTGTGTTCTCTGAGCTGGGTGCTTCTCCAGAGCTCCAGGAG
 GTCTCTCTCAGGATTTGTGAAACAAATGAAACAAATTAGAGCAAGCTGACTGGAGCCTCAGGAGGACAA
 ACATCATCTCCACTGACTCTTAGCCACTGCTTCTCTCTGTGCCATCCACTCCACCAACAGGTGTGTTTGGC
 CTGAGGAGCAGCCCTGCTGTCTCTTCTCCCACTTGTGATCAGGAAGTGGAGGAGCCAGGAGTGTCTT
 GTGGAGGACAGCAGTGGCTGCTGGGAGAGGGCTGTGGAGGAAGGAGCTTCTGGAGGCCCTCTCAGCTTACTCT
 GGGCCCCCTCTCTAGAGGAAGCTCAACTCTCTCCCACTCACCATTGGAAAGAAATATATGAATGCCACTG
 AGGCTCTGAGGCCCTACTCATGCAAAACAGGGTTCAAGGCTGGGTACGCAAGTGTGAGGAGGAGGAGG
 TATGAGACCGTAGGTCAAAGACCATCTCTGACTGTGTCTACTATGAGCTTAAAGAAATTTGATACCATAAAT
 GTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

0970166.101501

FIGURE 77

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404
<subunit 1 of 1, 985 aa, 1 stop
<MW: 105336, pI: 6.55, NX(S/T): 7
MGGMAQDSPPQILVHPQDQLFQGGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLLP
DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM
VAVVGEQFTLECGPPWGHPTEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAESDEGYMCV
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDAEGPKPRPAVWLSWKV
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG
PDSNVLLLRLEPKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNSTLPP
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGWP
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRTSEDAILKHRMD
HSDSQWLADTWRSTSGSRDLSSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTST
FYGLIAELPSSPTPARSPQVPVVRRLPPQLAQLSSPCSSSDSLCSRRGLSSPRLSLAPAEA
WKAKKKQELQHANSSPLLGRSHSLELRACELGNRGSKNLSQSPGAVPQALVAVRALGPKLLS
SSNELVTRHLPAPLFPFHPETPTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPSPQASS
LSGSPSPASSRLSSSSSLSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY
GYISVPTASEFTDMGRTGGGVGPKGVLLCPPRPCLTPTPSEGLANGWSASEDNAASARA
SLVSSSDGSFLADAHFARALAVAVDSFGFGLPREADCVFIDASSPPSPRDEIFLTPNLSLP
LWEWRPDWLEDMEVSHQTRLGRGMPPWPDSQISSQRSQLHCRMPKAGASPDYS

Important features:

Transmembrane domain:

amino acids 448-467

N-glycosylation sites:

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

N-myristoylation sites.

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

Phosphotyrosine interaction domain proteins

amino acids 740-753

FIGURE 78

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTGCCGTCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTGGAAGGGGACACTGTGT
 CCTCTGCATGCACCTACAGGGAAGAGCTGAGGGACCCCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTTCTCTCGTGTCTTGGCACCATTATGCAGAAGAAGAAGGCCAGGAGACAAT
 GAAGGGCAGGGTGTCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTTGTGACCTTGTGGA
 ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGTCGAAAAACCGGGGCCCGATGAG
 TCTTTACTGATCTCTCTGTTCTGTCTTTCAGGACCCCTGTGTCTCTCCCTCCCTCTTCCCAC
 CTTCCAGCCTCTGGCTCAACAACGCTTGACGCCCAAGGCAAAGCTCAGCAAAACCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAAGCAGGGGAAGACAGG
 GCTGAGGCCCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCCAGCGACCTCTCTCTGCGAGGAGCTCCGCCCCCCCATGCAGC
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG
 GTGTCCATCCCGATGGTCCGCATCTGGCCCCAGTCTGTGGTCTGCTGAGCCTTCTGTACGC
 CGCAGGCTGATCGCCTTCTGCAGCCACCTGCTCTGTGGAGAAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCCTTGACTGCGGAGGAAAGGAAGCC
 CTTCCAGGCCCTGAGGGGACGTGATCTCGATGCCTCCCTCCACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTTGGCCAGGCCAGAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCTCTCAGAG
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCAACCTCCCGAGGCTCTCTCTGTGATGTTTCCA
 GCCTGACCTAGAACGCTTTGTGAGCCCTGGAGCCCAGAGCGGTGGCCTTGTCTCTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGAACTCCTGGGC
 CTCATGCCCAGTGTGGACCCCTGCCTTCTCCACCTCCAGACCCACCTTGTCTTCCCTCCC
 TGGCCTCTCAGACTTAGTCCACCGGTCTCTGCATCAGCTGGTGTGATGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATCTGGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT
 GTGAAAAACGTGATTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTCTAACAATGCCCAGTGACTGTCGCACTTGAGTTTGAAGGCCAGTGGGCCGTG
 ATGAACGCTCACACCCCTTCAAGCTTAGAGTCTGCATTGGGCTGTGACGCTCTCCACCTGCC
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTTGGGACTCCCTCTGAGGCCCTGCTAAG
 TCCAGGCCCTTGGTCAAGTCAAGGTGCACATTGCAGGATAAGCCAGGACCGGCACAGAAAGTGG
 TTGCCCTTTNCCATTTGCCCTCCCTTGGNCCATGCCTTCTTGCCTTTGGAAAAAATGATGAAGA
 AAACCTTGGCTCTCTTGTCTGGAAAGGGTTACTTGCCTATGGGTTCTGTGTGGCTAGAGA
 GAAAGTAGAAAAACAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA
 GCACAACTACTATTTTCTTTTCTTTTCCATTATTATTTTAAAGACAGAATCTCGTGCT
 GCTGCCCAGGCTGGAGTGTGAGTGGCAGCATCTGCAAACTCCGCTCTCTGGGTTCAAGTGAAT
 CTTCTGCCTCAGCCTCCCGATAGCTGGGATTACAGGCACGCACCACCACACCTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATGTTGGCCAGGCTGGTCTTTGAACCTCCTGAC
 CTCAAATGAGCCTCTGTCTTCACTCTCCCAAATTGCGGGGATTACAGGCATGAGCCCTGCTG
 TCTGGCCCTATTCTTTTAAAGTGAATTAAGAGTTGTTTCAATGCAAACTTTGGAAG
 ATGGAGGAGAAAAAGAAAAAGAAAAAATGTCAACCATAGTCTCACCAGAGACTATCAT
 TATTTCGTTTGTGTACTTCTTCCACTCTTTCTCTTACATAAATTTGCCGGTGTCTT
 TTTACAGAGCAATTATCTTGATATACAACCTTGTATCTGCTCTTTCCACCTTATCGTTCC
 ATCACTTTATTCCAGCACTTCTCTGTGTTTTACAGACCTTTTTATAAATAAATGTTTCATCA
 CCTGCATAAAAAAAAAAAAA

09978165-16501

FIGURE 79

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALLEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRCGGILFSRCS
GTIYAEEEGQETMKGRVSIIRDSRQELSLIVTLWNLTLDAGEYWCGVEKRGPDSELLISLFV
FPGPCPPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEPPLPG
TSQYGHERTSQYTGTSPHPATSPPPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAAEKEAPSQAPEGD
VISMPPLHTSBEELGFSKFVSA

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

00703.10507

FIGURE 80

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA
GCCGCAGAGCCAGAGCAGACAGCCGAGAAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC
GCTCTGTTGCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACACGAGGGCTGGTGAGCTGCCTGTATCCAA
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGCATAGAAGCCAGGAG
CAGGGCTCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGC
TCAGCTGCCTGCTACCCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACCTGGCCAGAGTG
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCCTTGC
TTATTTCAACGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCGAACGTCCCCAAC
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTACTGGGAGGCCTGGAGGCATCACTGCC
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTTAGGATGGACGGAACCATGCA
CAGCAGGCTGGGAAATGTGTTTGGTTCTTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA
AAGGATGGTTGAACGTGAAA

097813310501

FIGURE 81

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD
YEADGSTNNGIFQINSRRWCNSLTPNVPNVCRCMYCSDLLNPNLKDTVICAMKITQEPQGLGY
WEAWRHHCQGKDLTEWVDGDCF

Important features:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homolgous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

09/03/2001 11:50:11

FIGURE 82

AGCCGCTGCCCCGGGCCGGGCCCGCGCGGCACCATGAGTCCCGCTCGTGCCCTGCGTTTC
GCTGCGCCTCCTCGTCTTCGCCGTCTTCTCAGCCGCCGAGCAACTGGCTGTACCTGGCCA
AGCTGTGTCGTCGGTGGGAGCATCTCAGAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATC
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGTGTGCGCCGCGGTGC
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCCGGAACCGGCGCTGGAAGTGTCTCCACAC
TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGAAGTCCGGAGGCGGCCCTTCGTG
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAAGTGACGCGGGCTGTCAGCAGTGGGGAGCT
GGAGAAGTGCGGCTGTGACAGGACAGTGCATGGGTCAGCCACAGGGCTTCAGTGGTCAG
GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG
AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACATGAGGCGGGCAG
GAAGGCCATCTGACACACATGCGGGTGAATGCAAGTGCCACGGGGTGTGAGGCTCCTGTG
AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCGCCAGGTGGGTACGCGACTGAAGGAG
AAGTTTGATGGTGCCACTGAGGTGGAGCCAGCGCGGTGGGCTCCTCCAGGGCACTGGGTACC
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG
ACTTCTGTGAGCAGGACATGCGCAGCGGCTGTGGGCACGAGGGGGCGCACATGCAACAAG
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGCGGCTTCACACGGCGCA
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAAATCCACTGGTGTGCTTCTGTCAAGTGCCGGC
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGAACCGCCTGCCTAGCCCTGCGCCGGC
AACCACCTAGTGGCCAGGGAAGGCCGATAATTAAACAGTCTCCACCACCTACCCCAAGA
GATACTGGTGTATTTTTTGTCTGTGTTTGGTCTTCTAGTGTATTTATTGCCGAA
ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAAGCCTTGGGCTTTGTGGCT
GCCACTGACCAAAGGGACCTTGCTCGTGCCGCTGGCTGCCCGCATGTGGCTGCCACTGACCA
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGCAGACCTAAGGTGGAGTAACAAGGAGTAT
TACCACCACATGGCTACTGACCGTGTATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATA
GGTACCGACTTGATGGAAGTCAACCCCTCTGGAAGGCAAGTCTTAACTCTCCAGCACACA
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG
GAACAAGCAGATACCAAGGTCAAGGGCACCAAGTTCAATTCAGCCCTTACATGGACAGCTAGA
GGTTTCGATATCTGTGGGTCCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA
GTCCACCCTAGAACCCAGCCTGCCCCAGCCTGCCCTGGGAAGAGGAAACTTAACCACTCC
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCCTT
TGCACTATGCCCCAGTCACTTTTACAGCGCTGTTTCCCTCCATGAAACTGAAAAACACACAC
ACCTGCGAGA
GAGAGGGAGGAAAGGGCTGTGCCCTTTGCAAGTCATGCCGAGTCACCTTTACAGCACTGTTCTC

09978108.101501

FIGURE 83

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRQVQMCKRNLE
VMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSAGVAFV
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSJNIAYGVAFSQSFVDVRERSKGASSSRALM
NLHNNEAGRKAILLTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRR
VGSSRALVPRNAQFKPHTEDELDVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC
CGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT
CGCCATGAGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGC
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCTCTGGTC
ACCACAGTCTCTTGGGCTGTGATTCTGAGTATCTATTGTCCAAGGCCTCCACGGAGCGCGC
GGCGCTGCTTGACGCGCCACGACCTGCTGAGGACAAACGCCCTCGAAGCAGACGGCGCGCTGG
GTGCCCTGAAGGAGGAGGTGCGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT
GCGGGAACCTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGCGAGGGGCCGTGAGGACG
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCTGCGAGCCG
TGCCCCACGTCGTGGCTGTCTTTCGAGGGCTCCTGCTACTTTTCTCTGTGCCAAAGACGAC
GTGGGCGGCGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC
TGGATGAGCAGGGCTTCTCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGG
GCTGTGCGCCATCTGGGCAAGGTTTCAGGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTT
CAGCCACTGGAACCAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTCTATGATGC
TGACACCGGGGCTGTGGAACGACGCAACGCTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG
AAAAGGCACAACCTGCTGA¹CCCCGCCAGTGCCCTGGAGCCGCGCCCATTCAGCATGTCTGTA
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTTCTTCCT
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC
TGGGCTCTGGGACCTCCATGCCGACCTCATCTAACTCCACTCAGCAGACCCAACTAACCC
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAA
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTCTCGCATTTTCCACCAAACCTGGA
AGCTGTTTTTGCAGCTGAGGAAGCATCAATAAATATTGAGAAATGAAAAAA

0993633.101501

FIGURE 85

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352
<subunit 1 of 1, 293 aa, 1 stop
<MW: 32562, pI: 6.53, NX(S/T): 2
MDTTYRSKWGGSSEEVPGGPWGRVWHSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA
LLDGHDLLRTNASKQTAALGALKEEVGDCHSCSGTQAQLQTTRAELGEAQAKLMEQESALR
ELRERVTTQGLAEAGRGREDVRTELFRALAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTW
AAQDHCADASAHLVIVGGLEQGFILTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS
HWNQGEPNDAWGRENQVMMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:

Type II transmembrane domain:

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

00070303 101501

FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCG
 GCAGCCCCCGCCGCCCGCAGCCCCCTTCTCTCTTTCTCCACGTCTATCTGCCTCTCG
 CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGAACTGGAGCCTCATTGGCCGGCCCCG
 GCGCCCGGCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCGACCGCTGCCGGC
 CGCGCTCCCGCTGCTCTGCGGGGTATGGAAAACCCCGACCCCGCCCGCCCTGGGCAAG
 GCCCTCTGCGCTCTCTCTCTGCGCACTCTCGGCGCCCGCGGCCAGCCTCTTGGGGGAGAGTC
 CATCTGTTCCGCCAGAGCCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA
 CGGCCTTCCCCAAGCAGTACCCCCCTGTTCCGCCCCCTGCGCAGTGGTCTTCTGCTGCTGGGG
 GCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTAGTAACGGGCTGCG
 CGACTTTGCGGAGCGCGGCGAGGCCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGAGG
 CGCTGCAGAGCGTGCACGAGGTGTTTTGCGCGCCCGCCGCTCCCGAGCGGCACCGGGCAGACG
 TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGCTCTGCTTTGTGGTGCGCATCGTGCC
 CAGCCCCGACTGTTCTGTTGGCGTGGACAGCCTGGACCTGTGCGACGGGACCGTTGGCGGG
 AACAGGCGGCGCTGGACCTGTACCCCTACGACGCGGGACGGACAGCGGCTTCACCTTCTCC
 TCCCCCAACTTCGCCACCATCCCGCAGGACACGCTGACCGAGATAACGTCCTCTCTCCAG
 CCACCGGCCAACTCTTCTACTACCCGCGGCTGAAGGCCTGCTCTCCATCGCCAGGGTGA
 CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCTGCCAGC
 AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCAGAAACGCCGCTGGACTGCGAGGTCTC
 CCTGTGGTCTGCTTGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA
 CTCGTACGTCGGGTCCAGCCCGCAACAACGGGAGCCCTGCCCGAGCTCGAAGAAGAG
 GCTGAGTGCCTCCCTGATAACTGCGTCTAAGACCAGAGCCCCCGAGCCCTGGGGCCCCCG
 GAGCCATGGGGTGTGCGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCGGAGGGCACAGGG
 GGTTCGCGCTGCTCTGACCGCGGTGAGGCCGCGCGGACCATCTCTGCACTGAAGGGCCCT
 CTGGTGGCCGCGACGGGCATTGGGAAACAGCCTCTCTCTTCCCAACCTTGCTTCTTAGGGG
 CCCCCGTGTCCTGCTCTCAGCCTCTCTCTCTGACAGATAAAGTCATCCCCAAGGCTC
 CAGCTACTCTAAATTATGTCTCTTATAAGTTATTGCTGCTCCAGGAGATTGTCTTATCAG
 TCCAGGGGCTTGCTCCACGTGGTTGCGAGATACCTCAGACCTGGTGTCTAGGCTGTGCTG
 AGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTGAATAAATGGGGCGG
 TTTGGAAGCGTCAGTGTTCATGTTATGGATCTCTCTGCTTTGAATAAAGACTATCTCT
 GTTGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

09/21/95 10:51

FIGURE 87

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPL
FRPPAQWSSLLGAHSSDYSMWRKNQYVSNGLRDFAEERGEAWALMKEIEAAGEALQSVHEVF
SAPAVPSGTGQTSAELEVRHSLVSFVVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYP
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP
RAFIPPAFVLP SRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGTKSRTRYVRVQPA
NNGSPCPELEEEAECPDNCV

Important features:

Signal peptide:

amino acids 1-26

0973433-101501

FIGURE 88

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTGTTGGTGTCCCTGTCTTGCGTGA
TATTGACAACTGAAGCTTTCTGCACTGACTTAAGGAAGAGTGTACTCGTAGGCGGA
CAGCTTTAGTGGCCGGCCGGCCGCTCTCATCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC
CAAGATGAGCAACATCTACATCCAGGAGCCTCCACGAATGGGAAGGTTTTATTGAAACTTA
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAGCTCTTAAAGCTTGCAGAAATTTT
ATCCAACCTTTGTTTGGAGCTTATTATGACAATACCATTTTTTCATAGAGTTGTGCCGTGGTTT
CATAGTCCAAGGCGGAGATCCTACTGGCAGAGGAGTGGTGGAGAGTCTATCTATGGAGCGC
CATTCAAAGATGAATTTCAATTCACGTTTGCCTTTTAATCGGAGAGGACTGGTTGCCATGGCA
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACACTGGGTCGAGCAGATGAAT
TAACAATAAGCATAACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAGCTGT
GAGGTTTTGTTTAAATCCTTTTGTATGACATCATTTCCAAGGGAAATTAAGGCTGAAAAAGA
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAATTTTAGTTTACTTTT
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG
GGCAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCAGT
TGTAAGAAAGTAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG
AGCATGATGAATATATTGATGGTGTATGAAAAGAACCTGATGAGAGAAAGAATTGCCAAAAA
TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC
AGTCAGCCGAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAACGGGAACCTCTTAGCAG
CAAAACAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAGAAAGTGAAGAGGAAGAA
GCCCTCCAGATGGTGTCTGTGCGCAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTTGAG
GAAGCAACAGTCAAAGAAGGGAACTTCCCGGGAAGATCAGACCCTTGCACTGCTGAACCAGT
TTAAATCTAACTCACTCAAGCAATGCTGAAAACCTGAAAAATGACATTCCTGAAAACAGAA
GTAGAAGATGATGAAGGATGGATGTACATGTACTTCAGTTTGAGGATAAAAGCAGAAAGT
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA
ATAAAGAAGGAGGGGAAGAAAGCAAAAGCTGATGAGAGAGAAAAAGAAAGAAGATAAAT
GAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTTGTAACAGCCATTG
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTGAACCTGTTGTCTGGTTTTG
AAAAACAATTATCTTTGTTTGGCAAATTGTGGAATGATGTAAGCAAAATGCTTTTGGTTACTGG
TACATGTGTTTTTCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCTCT
TCCACAAAAA

10501" 2212/960

FIGURE 89

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919
><subunit 1 of 1, 472 aa, 1 stop
><MW: 53847, pI: 5.75, NX(S/T): 2
MSNIYIQEPPTNGKVLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYDNTIFHRVVPGFI
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN
NKHTIFGKVTGDTVYNMLRLSEVDIDDERPHNPHKIKSCEVLFPNPFDDIIPREIKRLKKEK
PEEEVKLKPKGTKNFSLLSFGEAEAEAEAEAEVNRVSQSMKGKSKSSHDLKDDPHLSSVPVV
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKSV
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAEAPPDGAVAEYRREKQKYEALRK
QQSKKGTSREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMShVLQFEDKSRKVK
DASMQSDSTFEIYDPRNPVNKRREESKKLMREKKERR

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTTCGCCAGGTCGTCGCCGGCGAGAGAGATGCTGCCCGG
 CCCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCAGACCCATTTGCGCTTGCTGACGGCGTCTG
 AGCCCTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC
 GTGGCCCGCCGGCGGGACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGCTCTAGCAA
 CCCTTCTGTGGGCTCAATTTTGGAAATCTTGAAGTACTTCAACTCCAGCAACTACATCTG
 CTCCTTCAAGTGGTTTTTGAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA
 GGAGGAACAAATACAGGTGCCTTGACACCAAGAGGCCTCAAGTGGTCAACAAATATGGAAC
 CCTGCAAGGAAAAAGATGTCATGTGGGGAAGACACCCATCCAAGTCTTTTAGGAGTCCCT
 TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGACCTCCAGAACCCCGGAGCCCTGGAAA
 GGAATCAGAGATGCTACCACCTACCCGCTCGGATGGAGTCTCGCTCTGTGCGCCAGGCTGGAG
 TGCAGTGGCACGATCTCGGCTCACTGCAACCTCCGCTCCCGGGTTCAAGCGAGTCTCCTGC
 CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTCTGGGGCCAGCTGGCCTCG
 ATGTACGCTCAGCACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT
 GAACGTGTACGCGCCGCGCGCGCCCGGGATCCCCAGCTGCCAGTGTATGGTCTGGTTCC
 CGGGAGGGCCTTATCCTGTGGGCGCTGCTTCTTCGTACAGAGGCTCTGACTTGGCCGCCCGC
 GAGAAAGTGGTGCTGGTGTCTCTGCAGCACAGGCTCGGCTCTCTGAGCACGGA
 CGACAGCCACGCGCGCGGGAACCTGGGGCTGTCTGGACCAGATGGCGGCTCTGCGCTGGGTGC
 AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAATGTGACCTCTGTGCGCCAGTCCGCG
 GGGGCGATGAGCATCTCAGGACTGATGATGTACCCCTAGCCTCGGGTCTCTTCCATCGGGC
 CATTTCCAGAGTGGCACCGCGTTATTAGACTTTTCATCACTAGTAACCCACTGAAAGTGG
 CCAAGAAGGTTGCCACCTGGCTGGATGCAACCACAACAGCACACAGATCTGGTAAATGCTC
 CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTTCTCCAAC
 GAACCTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG
 TGATCCAGATGACCCCTTTGGTGCTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT
 CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCTTATAATATCACAAGGAGCAGGT
 ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGATGGAAGATGCTACGAA
 ACCGTATGATGGACATAGTTCAAGATGCCACTTTCTGTATGCGACACTGCAGACTGCTCAC
 TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA
 AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGAGCTCAAGGAGAAGAAGATGGC
 TTTTGGATGAGTCTGTACAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC
 TATGCAGGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGACTAGCCA
 TGGACATACCTGGGGACAAGAGTTCTACCCACCCAGTTTAGAATCTGCAGGAGCTCCCTGCT
 GCCTCCAGGCCAAAGCTAGAGCTTTTGCTGTGTGTGGGACCTGCAGCTGCCCTTTCCAGCC
 TGACATCCCATGATGCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC
 ACCACACTGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTCCTTTTCAAAATCCT
 CCCACCCCTTCAATGCTCTCCTTGTGACTCCTTCTTATGGGAGGTGACCCAGACTGCCACTGC
 CCCTGCTACTGCACCCAGTCTGGCAATTACCATCATCTGCTCAACCTTTTGTCTGTCTGT
 TCACATTGGCCTGGAGGCTTAGGGCAGGTTGTGACATGGAGCAAACTTTTGGTAGTTGGGA
 TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCAAAGTCTATACACAGGGGTG
 TCTCTTCAATAAAGAAGTGTGATTAGAAAAA

09781810501

FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179
<subunit 1 of 1, 545 aa, 1 stop
<MW: 58934, pI: 9.45, NX(S/T): 4
MSTGFSFGSGTLGSTTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTAPSSG
FGTGLFGSKPATGFTLLGNTGALHTKRPQVVTKYGTLLQKQMHVGTKPIQVFLGVFFSRPP
LGILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS
VWGYRCLQESWGLASMYVSTRERYKWLRFSEDCLYLNIVYAPARAPGDPQLPVMVWFPGGAF
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLDQMAALRWVQENIA
AFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA
HLAGCNHNSTQILVNCLRALSGTKVMRVS NKMRFLQLNFORDP EEI IWSMSPVVDGVVIPDD
PLVLLTQGKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMMD
IVQDATFVYATLQTAHYHRET PMMGICPAGHATTRMKSTCSWILPQEWA

Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

00978100 101501

FIGURE 92

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT
GCTGTCTCGTCTCTGGGCGGGTCCAGGCTATGGATGGGAGATTCTGGATACGATGCGAGG
AGTCAGTGATGGTGCCGAGGGCCCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCGGA
CAAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC
CAAGGGTGCTCCTGTGGGCCACAAACACAGAGTCGAGAGGTGGAAAAAGAGCACCGGGGGCC
GATTCAGACTCTGGGGATCCCGCCAAAGGGAACTGCTCCTTGGTGATCAGAGACGCGCAG
ATGCAGGATGAGTACAGTACTTCTTTGCGGTGGAGAGAGGAAGTATGTGACATATAAATT
CATGAACGATGGGTTCTTTCTAAAAGTAACAGTGCTCAGCTTCACGCCAGACCCGAGACC
ACAACACCCGACCTCACCTGCCATGTGGAATTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC
GTCCGACTCCGTGTGGCCATGCCCCAGAGACCTTGTATCAGCATTTCAGTGACAAACAC
GCCAGCCCTGGAGCCCCAGCCCCAGGAAATGTCCATACCTGGAAGCCCAAAAGGCCAGT
TCCTGCGGCTCTCTGTGCTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTGCGAG
AACAGAGTCTCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGG
GGTGAAGGCTGGGGATTCAAGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCAGC
AGCGAGCCCTGGACCTCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGTTTCCCAA
GCAAAACAGGACAGTCTCTGGAAAAACCTTGGGAACCGGCACGCTCTCCAGTACTGTGAGGGCCA
AAGCCTGTGCTGGTCTGTGTACACACAGCAGCCCCCAGCCAGGCTGAGCTGGAGCCAGA
GGGGACAGGTTCTGAGCCCTCCAGCCCTCAGACCCCGGGGTCTCGAGAGTGCCTCGGGTT
CAAGTGGAGCACAAGGAGGTTCACTTGCCACGCTCGGCACCACTAGGCTGGGCTCCAGCAGT
CTCTCTCAGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAG
CGTTTCTGGGAATCGGCATCAGGCTCTTCTTTCTCTGCTGGCCCTGATCATCATGAAG
ATTCTACCGAAGAGACGAGTACAGACAGAAACCCGAGGCCAGGTTCTCCGGCACAGCAC
GATCTTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAGCGGAATCAGA
AAGCCACACCAAAACGATCCTCGGACCCCTCTCCACAGGTGCTCCTCCCCAGAATCAAAG
AAGAACCAGAAAAAGCAGTATCAGTTGCCAGTTTCCAGAACCCAAATCATCCACTCAAGC
CCCAGAATCCAGGAGAGCCAAAGAGGAGTCCATTATGCCACGCTCAACTCCAGGCGTCA
GACCCAGGCTGAGGCCCGGATGCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTC
CAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGAGGGAAGGTAGAGTAAGAG
GTTGAAGATAACAGAGTGCAAAGTTTCTCTCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT
CTCTCTTTCTCTCTCTTTAAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCGTGAATC
CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGTTCGGGAGTTTCGAGAGGACGCTG
GCCAACTTGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGTGGCAGG
CGCCTGTAATCTTACCTACTTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG
AGGTTGCAGTGAGCCAAGATCACACCATTGACGCCAGCCTGGGCAACAAAGCGAGACTCCA
TCTCAAAAAAAAATCTCCAAATGGGTTGGGTGTCTGTAATCCAGCACTTTGGGAGGCTA
AGGTGGTGGATTGCTTGAGCCAGGAGTTCGAGACCAGCCTGGGCAACATGGTGAACCC
ATCTCTACAAAAATACAAAAACATAGCTGGGCTTGGTGGTGTGTGCTGTAGTCCAGCTGT
CAGACATTTAAACAGAGCAACTCATCTGGAATAGGAGCTGAATAAAAATGAGGCTGAGACC
TACTGGGTGCATTCTCAGACAGTGGAGGCATTCTAAGTCAAGGATGAGACAGGAGGTCCG
TACAGATACAGTCAATAAGACTTTGCTGATAAAAACAGATTGCAGTAAAGAACCCAAACCA
ATCCACCAAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCTCTCTCACTGCTACACTCTT
GACAGCCACATGACAGTTTACAAATGCCATTGGCAACATCAGGAAGTTACCCGATATGTCCCA
AAAGGGGGAGGAATGAATAATCCACCCCTTGTGTAGCAATAAGCAAGAAATACCATAAAA
GTGGGCAACCAGAGCTCTAGGCGTGCTCTTGTCTATGGAGTAGCCATTCTTTGTCTCTT
TACTTTCTTAATAAATCTGCTTTACCTTAAAAAAA

060718138 10150

FIGURE 93

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002

><subunit 1 of 1, 544 aa, 1 stop

><MW: 60268, pI: 9.53, NX(S/T): 3

MLLPILLSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYWFK
AVTETTKGAPVATNHQSREVMSTRGRFQLTGDPKAGNC SLVIRDAQMDESQYFFRVERGS
YVTYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS
ISRDNTPALEPPQPGNVPLYEAQKGQFLRLCAADSQPPATLSWVLQNRVLSSSHWPWGPRPL
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLNGTSL
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHP
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLLFLCLALIIMKILPKRRTQTETPRPR
FSRHSTILDYINVVPTAGPLAQKRNQKATFNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEP
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

Important features:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

Immunoglobulins and major histocompatibility complex proteins signature.

amino acids 365-371

FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAACTGTTATTTACTGCTGCGTTT
TATGTTGGGAATTCCTCTCCATATGGCCCTTGTCTTGGAGCAACAGAAAACTCTCAAAACAAAGA
AAGTCAAGCAGCCAGTGGCATCTCATTTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT
TTTGTACCAAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA
CAATGGAAACAATTCCTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGGAAGTACTTTTATCA
TTGATGAAAGAACAGGTGA CATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC
TACATCTTAAAGACCCAGGTAAATAGACATCGCTACTGGAAGGGCTGTGGAACTGAGTCTGA
GTTTGTCTCAAGATTTTCGATATCAATGACAATGAACCAAAATCCCTAGATGAACCTTATG
AGGCCATTGTACCAAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCGATGAT
GCTGACGATCCCTCAAGTGGTAATATGTCTGCTCTCTACAGCTTACTTCAAGGCCAGCC
ATATTTTTCTGTGTAACCAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC
TGCAAGATGAGTATTGGGTAACTATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG
TCTGGAACAACAAGTGTAATTAATTAACCTTTCCAGATGTTAATGACAAATAGCCCTATATTTAA
AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA
TCAATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTTGAAGAGGAT
GATTGCGCAACATTTGACATTTATTAATACTAATCATGAACTCAAGGAAGGATAGTTTATATTA
AAAGAAAGTGGATTTTGGAGCACCAGAACCCTACGGTATTAGAGCAAAAGTTAAAAACCATC
ATGTTCTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCACTTTTCAATTAAGATCCAG
GTGGAAGATGTTGATGAGCCCTCTCTTTTCTCTCTTCAATATGATTGATTGAAAGTTTGA
AGAAACCCACAGGGATCATTTGAGGCGTGGTGTCTGCCACAGACCAGACAATAGGAAT
CTCTCATAGGTATCTTACTAGGAGCAAAGTGTTCAATATCAATGATAATGGTACAATC
ACTACAAGTAACCTCAGTGGATCGTGAATCAGTGTCTGGTACAACCTTAAGTATACAGCCAC
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAAACATCA
ATGATCATGCTCTTGAGTTCTCTCAATACTATGAGACTTATGTTTGGAAATGCAAGCTCT
GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATT
TTACTTTAATCTATCTGTAGAAGACATAACAATTCAGTTTTCATATCATAGATAATCAAG
ATAACACAGCTGTCTATTTGACTAATAGAACTGGTTTAACTTCAAGAAGAACCTGTCTTC
TACATCTCCATCTTAATTTGCCGCAATGGAATCCCGTCACTTACAAGTACAACACCCCTTAC
CATCCATCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG
TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTGTGCATTATGATCATA
TTTGGGTTTATTTTGTGCTTTGGGTTTAAACACACGGAGAAAAACAGATTCTATTTCTCGA
GAAAAGTGAAGATTTACAGAGAAATATATCCAATATGATGATGAAGGGGGTGGAGAAGAAG
ATACAGAGGCCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATCGGGAACGCAAGACT
CGGAAACCAACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCGCA
CAGTGCCATATTCAGGAAATTCATCTCGAAAAGCTCGAAGAAGCTAATACTGATCCCGTGTG
CCCTCTCTTTGATTCCCTCCAGACCTACGCTTTTGGGGAACAGGGTCAATTAGCTGGATCC
CTGAGCTCTTGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT
GGGACCTCGCTTTAAAGATTAGCATGCATGTTTGGTTCTGCAAGTGCAGTCAAAATTAATAGG
GCTTTTACCATCAAAATTTTAAAGTGCTAATGTGATTGCAACCAATGGTATGCTTTAA
AGAGTTTTGTGCCCTGGCTCATATGGCGGGAAAGCCCTAGTCTTATGCGATTCTCTGATTCC
CTGGAGTAAATCTCCATGGTTATTTTAAAGTACCTACATGCTGTCTATTGAACAGAGATGTG
GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACAGGATTTGAAGTAAATTAATG
TAGGAAGATATTTAAAGTAGATAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT
CATTTATTTACTTAGGAAGAGTAAAAATACCAACAGGAAATTTAAAGGAGCAAAATTTG
CAAGTCAATAGAAATGTACAAATCGAGATAACATTTTACATTTCTATATGATGATGAA
ATTGAAATGTATAGTCAGAGAAATTTTATGAATTTATCCATGAAGTATGTTTCTTTTAT
TTAAA

FIGURE 95

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
><subunit 1 of 1, 772 aa, 1 stop
><MW: 87002, pI: 4.64, NX(S/T): 8
MNCYLLLRFMLGIPLLWPCLGATENSQTKVKQPVRSHLRVKRGVWNQFFVPEEMNTSHH
IGQLRSDLONGNNSFYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVSINDNEPKFLDEPYEAIVPPEMSPEGLTVIQVTASDADDPSSGNNARL
LYSLQGPYPYFSVEPTTGVIIRISSKMDRELQDEYVWIIQAKDMIGQPGALSGTTSVLIKLSD
VNDNKPIFKESLYRLTVSESAPTGTSGITIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
TQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL
PYVYFEVFEETPQGSFVGVSATDPDNRKSPYRYSITRSKVFNINDNGTITTSNSLDREISA
WYNLSITATEKYNIQEISSIPLYVQVLNINDHAFESQYYETYVCENAGSGQVIQTISAVDR
DESIEHHFYFNLSVEDTNSSFTIIDNQDNTAVILTNRTGFNLQEEFVFIISILIADNGIP
SLTSTNTLTIHVCDGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGLAGSLSSLESASVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

FIGURE 96

ATTTC AAGGCCAGCCATATTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTTNTA
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT
CAGCCAGGAGCGTTGINTGGAACAACAAGTGTATTAATTAACTTT CAGATGTTAATGACAA
TAAGCCTATATTTAAAGAAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC
AGCATTGAAGAGGATGATTGCGAAACATTTGACATTATT

0973/88-101501
105101-8812/660

FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCGGGCGCGGACCCCAACCCCGAC
 CCAGAGCTTCTCCAGCGCGCGCGCAGCGAGCAGGGCTCCCCGCGCTTAACCTTCTCCGCGGGG
 CCCAGCCACCTTCGGGAGTCCGGGTGCGCCACCTGCAAACTCTCCGCTTCTGCACTGCCA
 CCCCTGAGCCAGCGCGGGCCCCGAGCGAGTCTATGSCAACCGCGGGGTGCAGCTGTTGGGC
 TTCATTCTCGCTTCTCGGATGGATCGCGCCATCGTCAGCACTGCCCTGCCCCAGTGGAG
 GATTACTCTATGCCCGCGCAACAATCGTGACCGCCAGGCCATGTACGAGGGGTGTGGGA
 TGTCTCGGTGTCCGAGAGCACCGGGCAGATCCAGTGCAAACTCTTGACTCCTTGCTGAAT
 CTGAGCAGCAGTGCCAAGCAACCCGTGCCTTGATGGTGGTGGCATCCTCCTGGGAGTGT
 AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCCTTGGGAAGACATGAGGTGC
 AGAAGATGAGGATGGCTGTCTATGGGGGTGCGATATTCTTCTTGCAGGTCTGGCTATTTTA
 GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCTATGACCCCATGACCCAGT
 CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGTGCTGCTTCTCTCTGCC
 TTCTGGGAGGTGCCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCAACACCA
 AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAAGACTACGTTGACACAGAGGCAAAAG
 GAGAAAAATCATGTGTAAACAAACCAGAAATGGACATTGAGATACTATCATTAACTATTAGGAC
 CTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAAAACAACCAACAAAA
 ACCCATGTGTTAAATACCTCAGTGCTAAACATGGCTTAATCTTATTCTTCTTCTCTCA
 ATATAGAGGGGAAGATTTTCCATTGTATTACTGCTTCCATTGAGTAATCATACTCAAAAT
 GGGGGAAGGGGTGCTCCTTAAATATATATAGATATGATATATACATGTTTTTCTATTAAAA
 ATAGACAGTAAAAATCACTATTCTCATTTATGTTGATCTAGCATACTTAAATATCTCTAAAT
 AGGTAATGTATTTAAATCCATATTGATGAAGATGTTTATTGGTATATTTTCTTTTCGTCT
 TTATATACATATGTAACAGTCAAATATCATTTACTCTTCTTCAATGACTTTGGGTGCCCTTG
 CCACAAGACCTAGCCTAATTTACCAAGGATGAATCTTTCAATCTTCTCATGCGTCCCCCTTT
 CATATACTTATTTTATTTTACCATAATCTTATAGCACTTGCACTGTTTATAGCCCTTAT
 TTGTTTTGTGTTTTATTGGTCTCTATCTCTGAATCTAACACATTTATAGCCCTACATTTTA
 GTTCTAAAGCCAAGAAGATTTATACAAATCAGAACTTTGGAGGCAAACTTTTCTGCATG
 ACCAAAGTGATAAATTCCTGTTGACCTTCCACACAATCCCTGTACTGTACCCATAGCACT
 CTGTTTGTCTTGAANAATTTGTCCAAATGAGTAGCTGCATGCTGTTCCCCCAGGTGTTGT
 AACCAACTTTTATGATTGAATTTTAAAGCTACTTATTCTAGTTTTATATCTCCCTAAACT
 ACCTTTTTTGTTCCTTCTTAAATTTGATTGTTTTCCCAAGTGAATTTATCATGCGTTTTA
 TATCTTCTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA
 ATCTGGTGACAAATATTCTCTGTAGCTGTAAGCAAGTCACTTTTCTTCTACCTCTTTT
 TTCTATCTGCCAAATTTAGATAATGATACCTAACAGTTAGAAGAGGTAGTGTGAATATTAA
 TTAGTTTATATTACTCTTATCTTGAACATGAACATATGCCTATGTAGTGTCTTTTATTGTCT
 CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACGTACCTTCAATGTGAT
 CTAGCTCCTCTCTCTCTACCAAGTCTATTTCCTGAAACAAACCTACACACATACCTTCTAT
 GTGGTTCAGTGCTTCTCTCTCTACCAAGTCTATTTCCTGAAACAAACCTACACACATAC
 CTTCATGTGGCTCAGTGCTTCTCTCTCTACCAAGTCTATTTCCTTCTTCTCAGCTGTGTCT
 GACATGTTTGTGCTCTGTGTCATTTTAAACAACCTGCTCTTACTTTTCCAGTCTGTACAGAATG
 CTATTTCACTTGACCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAGACCTG
 GATTGTAGTCTTGTGTCTATCAATCACCGTCTGTGTTTGAGCAAGGCAATTTGGCTGTCTAA
 GCTTATGTCTTCACTCTGAACGGTGGTTTGTAAATCTCTGATCTTCCCACTCAGAGTATG
 TTGTGGGATCCAGTGAGATAGAATACATGTAAGTGTGGTTTTGTAAATTTAAAGTGTCTAT
 ACTAAGGGAAGAAATTTGAGGAATTAAGTGCATACGTTTTGGTGTGTCTTTTCAATGTTTGA
 AAATAAAAAAATGTTAAG

03972188-101501

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFI LAFLGWIGAI VSTALPQWRIYSYAGDNIVTAQAMYEG LWMSCV SQSTGQI
QCKVFD SLLNLSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDEDEVQKMRMAVIGGA
IFLLAGLAILVATAWYGNRIVQEFYDPMTPVFNARYEFGQALFTGWAAASLCLLG GALLCCSC
PRKTTSYPTPRPYPKPAPSSGKDYV

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

0070188110507

FIGURE 99

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG
TGACCGCCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTGCGAGAGCACCGGGCAG
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA
AGTGTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCTATTGGGGGC
GCGATATTTCTTCTTGCCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAN
CNTTCAACANTTCTATGACCCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCA
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTGGGAGGTGCCCTACTTTGCT
GTTCTGTCCC

0375188-101501

FIGURE 100

ACCCTTGACCCAACGCGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG
GCTTCATTCTCCCCCTTCCTGGGATGGACCGGCGCCCATNTCAGCACTGCCCTGCCCCAGTG
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCCAGGCCNTGTACGAGGGGCTGT
GGATGTCCTGCGTGTGCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAG
TGATAGCAATCTTNNTGGCCACCGTTGTNNNTGAAGTGTATGAAAGTGCTTGGAAGACGATGA
GGTGCAGAAGATGAGGATGGCTGTTCATTGGGGGCGCGATATTCTTCTTGCAAGTCTGGCTA
TTTGTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

FIGURE 101

GGGCCGACCATTATCCAACCGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC
CATCNTCAGACTCCCTGCCCCATGGAGATTNNCCTATGCTGGCGACAACATCNTGACCCCC
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTGCGAGANCAACGGGCAGATCCAGTGCAA
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT
TGGCATCCTCCTGGGAGTGATAGCAATCTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATTGGGGCGCGATATTTCTT
CTTGCAGGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT
TCTATGACCCATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC
TGGGCTGCTGCTTCTCTGCTTCTGGGAGGTGCCCTACTTTGCTGTTCTGCGA

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ATTCTCCCCTCCTGGATGGATCGCNCACCGTCACATTGCCCTCCCCCANTGGAGGATTNAC
TCCTATGCTGGCGACAACATCGTGACCCCCAGGCCATTACCGAGGGGCTTTGGATGTCNT
GCNTGTGCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG
CAGCACATTGCAAGCAACCCGTGCTTGTATGGGGTTGGGATCCTCCTGGGAGTGATAGCAAC
CTTTGTGGCCACCGTTGGCATGAAGTGATGAAGTGCTTGAAGACGATGAGGTGCCAGAAG
ATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTGTGTGACGGTCTGGCTATTTTAGTNGC
CACAGCATGGTATGGCAATAGANTNNNTTCNNGNNNTCTATGACCCCTATGACCCCAAGTCAATG
CCAGGTACGAATTTGCTAGGCTCTTTCACGCTTACGCTGGCTGGGCTGCTGCTTCTCTGCTCCTCTG
GGAGGTGCCCTACTTTTCTGTTCTCTGCTCC

FIGURE 103

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC
AAGCAACCCCTTGCCCTTGAAGGTGGTTGNCATCCCCCTGGGAGTGAATAGCAATCTTTGTG
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCAATGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTNNCCACAGCAT
GGTATGGCAATAGNATNNTTCGNGGNTTCTATGACCCCTATGACCCAGTCAATGCCAGGTAC
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTGGGAGGTGC
CCTACTTTGCTGTTCTGTCCCCGAA

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FIGURE 104

AGCAATGCCCTGCCCCAGTGGAGGATTAATTCCTATGNTGGGGACAACATTGTGACNGCCC
AGGCCATGTACGGGGGGCTGTGGATGTCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGC
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGATGA
AGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTT
CTTNTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAATNGTTCAAGA
ATTTTATGACCCATATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTTTNTTCACTG
GCTGGGCTGCTGCTTNTTTCTGCCTTNTGGGAGGTGCCCTANTTTGCTGTTCTGCGAACC

0997818.101504

FIGURE 105

TCATAGGGGGGCGCGATATTTTTCTTGCAAGTNTGGTTATTTTAGTTGCCACAGCATGGTA
TGGCAATAGAATCGTTCAAGAATTNTATGACCCTATGACCCAGTCAATGCCAGGTACGAAT
TTGGTCAGGCTCINTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA
CTTTGCTGTTCTCTG

0978488.101501

FIGURE 106

TTCTGGGATGGATCCGCCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC
TGGCGAACAAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT
TGCAAGCAACCNTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG
CCACCGTTGGCATGAAAGTGATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTGCTATTGGGGGCGGATATTTCTTCTTGCAAGTCTGGCTATTTTAGNNGCCACAGCAT
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCATGACCCAGTCAATGCCAGGTA
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG
CCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCACG

0070100-101501

FIGURE 107

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGGGCCATCGTCAGCA
CTGCCCTGCCCCATGGAGGATTACTCNTATGCTGGCGACAACATCGTGACCNCCCAGGCCA
TGTACGAGGGGCTGTGGATGTCNGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCT
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACNTGCCTTGATGGTGGTTGGCA
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGATGAAGTGCTTG
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTTCATTGGGGGCGCGATATTTCCTTGC
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT
GACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGC
TGCTGCTTCTCTGCTTCTGGGAGGTGCCCTACTTTGCTGTTCTTCGCGAA

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FIGURE 108

GCGTGCCGTCAGCTCGCCGGGACCCGCGGCCTCGCCCTCGCCCTCGCCCTCGCCCTCGCCCTCGC
 CGGTAGACCGACCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCCGCGCGTGC
 ACCGGTCCCCGCTTTTGTAAAACTTAAAGCGGGCGCAGCATTAACGCTTCCGCGCCCGGT
 GACCTCTCAGGGGTCTCCCGCCAAAGGTGCTCGCCGCTAAGGAACATGCGCGAAGGTGGAG
 CAGGTCTGAGCCTCGAGCCGCGAGCAGAGCTCAAATTCGAGGTCCTTCACCGATGTTGT
 CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTAAAGGTGAAGACTA
 CAGCACCACGTAGGTACTGTGTGAGGCCAACAGCGGAATCATCGATGCAGGGGCTCAAT
 AATGTATCTGTGATGTTACAGCCTTTCGATTATGATCCCAATGAGAAAAAGTAAACACAAGT
 TATGTTTCAGTCTATGTTTGTCTCAACTGACACTTCAGATATGGAAGCAGTATGGAAGGAGG
 CAAAAACCGGAAGACCTTATGGATTCAAACTTAGATGTGTGTTGAATTGCCAGCAGAGAAT
 GATAAACCATGATGTAGAAATAAATAAAATTATATCCACAACTGCATCAAAGA CAGAAAC
 ACCAATAGTGTCTAAGTCTCTGAGTCTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG
 AAGAATGTAAGAGGCTGCAAGGTGAAGTTGAGAGGCTACGGGAGGAGAACAGCAGTTCAAG
 GAAGAAGATGGACTCGCGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTAGCATTAGC
 CCAACTGGGAAGGAAGAAGGCTTAGCACC CGCTCTGGCTCTGGTGGTTTTGTTCTTTA
 TCGTTGGTGAATATTATGGGAAGATTGCTTGTAGAGGTAGCATGCACAGGATGGTAAATTG
 GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTA AAAAGAAATT
 AATGTATGATGACATCTCACAGGTCTTGCTTTAAATTAACCCCTCCCTGCACACACATACAC
 AGATACACACACAAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTG
 ATTGAGGGGGAAAAAGATGATCTTTATTATGACAAGGGAAACCATGAGTAATGCCAAT
 GGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGCTGGATTACCTC
 TCTTAAATGACACCCCTTCCCTCGCTGTTGGTGTGCGCCCTTGGGGAGCTGGAGCCAGCAT
 GCTGGGGAGTGCGGTGAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGCCAGGCTG
 CTTCCGTGTCTTCAGTCTGTCTCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA
 AGCCCAAAGGAATGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT
 TGACTGATTGACCCAGCGCTTTGGAATAAATGGCAGTGCTTTGTTCACCTTAAAGGGACCAA
 GCTAAATTTGTATTGGTTGATGAGTGAAGTCAAACCTGTTATTGAGAGATGTTTAAATGCATA
 TTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTACAAAGAGTACAGTTAATGC
 TGCCTGTCTGTAACCTGTGTTGGGTGAACCTGGTATTGCTGCTGGAGGGCTGTGGGGCTCCTCT
 GTCTCTGGAGAGTCTGGTCAATGTGGAGGTGGGGTTTATGGGATGCTGGAGAGAGCTGCCA
 GGAAGTGTTTTCTGGGTGAGTAAATAACAACCTGTATAGGGAGGGAAATCTCAGTAGTG
 ACAGTCAACTCTAGGTTACCTTTTAAATGAAGAGTAGTCAGTCTCTCAGATTGTTCTTTATA
 CCACCTCTCAACCATTAATCTCACACTCCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC
 TTGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC
 ACCAGAGTTGTGGGTGGGGAGCAAGGGGAAGAGAGAACTCTCAGCGAATCCTCTAGTAC
 TAGTTGAGAGTTTGACTGTGAATTAATTTATGCCATAAAAGACCAACCCAGTTCTGTTTGA
 CTATGTAGCATCTGAAAAGAAAAATTATAATAAAGCCCCAAATTAAGAAAA

0970158.10507
 10507.158.097

FIGURE 109

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHELKFRGPFSTDVVTNLKLGNPTRNVCFKVKTTAPRRYCVRPNSGIID
AGASINVSVMQLQPFDDPNEKSKHKFMVQSMFAPTDTSMEAVWKEAKPEDLMSKLRVFE
LPAENDKPHDVEINKIISTTASKTETPIVSKSLSSSLDDTEVKVMEECKRLQGEVQRLREE
NKQFKKEEDGLMRKTVQSNSPISALAPTGKEEGLSTRLLALVVLFFIVGVIIGKIAL

Important features:

Transmembrane domain:

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

09978332 101501
105101 89187660

FIGURE 110

GTCAGTCTTCTAGATTGTCCTTATCCCACCTTTCAACCANTACTCACATTTTCNAGCGCCCAG
GTCCANGTCTGAGCCTGACTTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTGAAAAGAAAAATTATAATAAGCC
CCAAAATTAAGAATTCCTTTGTCTTTTGTCTCATTTGCTCTATGGGGGAATTATTATTTT
ATCATTTTATTATTTTGGCATTGGAAGGTAACTTTAAATGAGC

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TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCCTTGGTACATGATGCTGGATTACCTCCTT
AAATGACACCNNTTCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCTGGAGCCCCAGCATGCTG
GGGAGTGGCGTCAAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCAGGCTGCTTT
CCGTGCTTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT
AAATTGTATTGGTTTCATGTAGTGAAGTCAAACCTGTTATTTCAGAGATGTTTAAATGCATATTTA
ACTTATTTAAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG
TGCTGCTGAACCTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

FIGURE 112

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAAATNTTGGGAAGATTGCTTGTAGAGGTA
GNATGCACCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAAACGATNTTTTAG
AAAGTTAAAAATGTATAGTAAC

09978133.101501

FIGURE 113

GGTGGCCCATTCCTCGGCCAGGCTGCTTTCCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC
TTGTNATAAGTGAGAGGCGTGTGTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT
GCTTTGTTTCAATTAAGGGACCAAGCTAAATTGTATTGGTTCATGTAGTGAAGTCAAACG
TTATTCAGAGATGTTTAAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACTGGTATTGC
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

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FIGURE 114

TGCTTTCCGTGTCCTTCAGTTCGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG
TGTTGACTGATTGACCCAGCGCTTTGGAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAGTGTATTTCAGAGATGTTTAATGC
ATATTTAACTTATTTAATGTATTTATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA
TGCTGCGTGC

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FIGURE 115

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAATGACAAGGGAAACNTGNGT
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC
TGGATTACCTCTCTTAAATGACACCCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN
GAGCCCAGCATGCTGGGGAGTGGGTCTGCTCCACACAGTAGTCCCCANGTGGCCANTCCC
GGCCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA
ACAGAGTCAGAAGCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTGGAAATAAATGGCAGTGCTTTGTTTCANTT
AAAGGGNCCAAGNTAAATTTGTATTGGTTCATGTAGTGAAGTCAAANTGTTATTTCAGAGATG
TTTAATGCATATTTAANTTATTTAATGTATTTTCATNTCATGTTTTTCTTATTGTCACAAGGGT
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

0973733-101504

FIGURE 116

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTGAGCTCCACACAGTAGTCCC
CACGTGGCCCACTCCCGGCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGC
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACG
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGC
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAA
CTGTTATTCAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTC
TTATTGTACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTAT
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTTCATGTGGAGGTGGG

09973138-10150

FIGURE 117

GCGAGCTCCGGGTGCTGTGGCCCGGCCCTTGGCGGGGCGGCCCTCCGGCTCAGGCTGGCTGAGA
 GGCTCCCAGCTGCAGCGTCCCCGCCCGCCTCCTCGGGAGCTCTGATCTCAGCTGCAGTGGC
 CTCGGGGACCAAAACAAGCCTGGCAGGGTCTCACTTTGTGGCCAGGCTGGAGTTTCACTGGCCA
 TGATCATGTTTACTGACGCTTGACCTCCTGGGTTCAGCGATCCTGCTGAGTAGCTGGGA
 CTACAGGACAAAATTAGAAGATCAAAATGGAAAAATATGCTGCTTTGGTTGATATTTTACC
 CCTGGGTGGACCTCACTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA
 GGTACCCCGGATTCTCAGTGAAAGGACTTTCATCTCACCAGCCCCGATTGTGAGGCAGATG
 CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCAGC
 CTTTCTGAATTGGAGGATTATCTTTCCCTATGAGACTGTCTTTGAGAATGGCACCCGAACTT
 AACAGGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG
 TATCTGTTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTTCACTCTTGGACAAA
 AGGTTCTTAAACAATTTCCCTTTTCAACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT
 TCTCATTTCCCTCAGCATGTTCTAACTGCTGCCACTGTGTTTCACTGATGGAAGGACTATG
 TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTGGAAGATGAGGAATAAAAGTGGAGGCAAG
 AAACGTCGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGGTGACAAAGAGAGGGTAC
 CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAAAAATCTGGCCGGGGTCT
 AGAGGATTGCCGAAGGGAGGCTTCTCTTTTCAAGTGGACCCGGGTCAAGAAATACCCACATTCG
 AAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTCTGGA
 GCTGAAGCGTGCTCACAAAAAGAAATACATGGAACCTTGAATACGCCCAACGATCAAGAAAA
 TGCCTGGTGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT
 CGGTTTTCAGTGTGTCCGACGAATCCAATGATCTCCTTTACCAATACGCGATGCTGAGTC
 GGGCTCCACCGGTTTCGGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAAGAAATTGGAAGC
 GCAAAATCATTTGGGCTTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTTCAAGGAC
 TACAACGTTGCTGTTTCGCATCACTCCCTTAAAAATACGCCAGATTGCTCTGGAATCACGG
 GAACGATGCCAATTTGTCTTACGGCTTAAACAGAGACCTGAAACAGGGCGGTGATCATCTAAA
 TCACAGAGAAAAACAGCTCTGCTTACCGTAGTGAGATCACTTCAATAGTTTATGCTGGACTT
 GAACCTCTGCAATAGCATTTCAACATTTTCAAAATCAGGAGATTTTCTGCTCAATTTAAAAAA
 TGATAGGTGCAGATATTGAAACTAGGTGGGCACTTCAATGCCAAGTATATACTCTTCTTTA
 CATGGTGATGAGTTTCATTTGTAGAAAAATTTTGTGCTTCTTAAAAATTAGACACACTTT
 AAACCTTCAAAACAGGTTATTAATAACATGTGACTCCTTAATGGACTTATTTCCAGGGTCC
 TACTCTAAGAAAGATCTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTCATAGATAAA
 GGTAGATGGTAAAGCAATTAGTATCAGAAATAGAGACAGAAAGTTCAACACAGTTTGTACTA
 CTCTGAGATGGATCCATTCACTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGTCT
 GGGACATTTAGTTTAGTTTTTTTGAAGAAATTCAAAATCAGAAAGAAAGCAAGCATTATATAA
 CAAAATAAATCTGTTTACTGCTTTAAGAAATAACAAATCAAAATGTGATTTATTTAAAAAA
 TGGGAGAAATAGTTGTTCTATGAAATAAACCTAGTTTGAAGAAAGGGAAGCTGAGACATTT
 TAAGATCTCAAGTTTTTATTTAACTAATACTCAAAATATGGACTTTTCATGTATGCATAGGG
 AAGACACTTCACAAATTAAGATGATCATGTGTTGAAAGCCACATTTTATGCTATATACAT
 TCTATGTATGAGGTGCTACATTTTGGAGCAAGAAATCTGTAATCTTTTCAAGAAAGAGT
 CTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGCTGAATTTCTCTGATTAG
 TAATTTTATAGATATGCTCTTCTTAAAAATGAATAAAATTTATGAATATGA

19975138.101501

FIGURE 118

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253
<subunit 1 of 1, 413 aa, 1 stop
<MW: 47070, pI: 9.92, NX(S/T): 3
MENMLLWLIFFTPGWTLLIDGSEMEDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVC
GIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQV
YGTDSRFSILDKRFLTNNPFFSTAVKLSTGCSGILISQHVLTAAHCVDGKDYVKGSKKLRV
GLLKMRNKSQGGKKRRGSKRSRREASGGDQREGTREHLQERAKGRRRKKSGRGORIAEGRPS
FQWTRVKNTHIPKGWARGMGMDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS
GFDNDRADQLVYRFCVSDSDNLLYQYCDAESGSTGSGVYLRKDPDKKNWKRKIIAVYSG
HQWVDVHGVQKDYNAVVRITPLKYAQICLWIHGNDANCAYG

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

007013101511

FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTAGCACCAGTACTGGAT
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTAGTGTCCGATTCTGATTCCGGCAAGG
ATCCAAGCATGGAATGCTGCCGTGGGCAACTCCTGGCACA CTGCTCCTCTTTCTGGCTTTC
CTGCTCCTGAGTTCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCCTCTACTCTCTGAGGCGCT
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATA CAGAACATGCAGTAATGTGGAC
TGCCCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA
AGTGCCAAAGCCAAAGGAACAACCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA
TCACCAGCTGGGAAGCACCGCTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA
CCTGCCGCTGGTCCGAGGGCAGTATAAATCCAGCTCTCCGCAACCAAATCGGATGATACT
GTGTTGTGCACTTCCCTATGGAAGTAGACATATTGCGCTTGTCTTAAAGGTCTCTGATCACTT
ATATCTGGAACCAAAAACCTCCAGGGGACTAAAGGTGAAAAACAGTCTCAGCTCCACAGGAA
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA
ATGGCTGGACCACTCACAGCAGATTTCAATGTCAAGATTCTGAATCGGGCTCCGCTGACAG
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC
CTTGCTCAGCAACCTGTGGAGGAGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC
CTTATGACCTCTACCATCCCTTCCTCGGTGGGAGGCCACCCATGGACCGCGTGCTCCTCC
TCGTGTGGGGGGGCATCCAGAGCCGGGCAGTTTCCTGTGTGGAGGAGGACATCCAGGGGCA
TGTCACTTCAGTGGAAGAGTGGAAATGCATGTACACCCCTAAGATGCCATCGCGCAGCCCT
GCAACATTTTTGACTGCCCTAAATGGCTGGCAGAGTGGTCTCCGTGCACAGTGACATGT
GGCCAGGCCTCAGATACCGTGTGGTCTCTGCATCGACCATCGAGGAATGCACACAGGAGG
CTGTAGCCCAAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA
AACCCTAAGAGAGAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA
GAAGAAGGAGCTGCTGTGTGAGGAGGCCCTCGTTAAGTTGTGTAAGCAGCAGACTGTTCTATA
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA
ACTAAGTGTAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAAGATTGATTAGTTTCAA
AAAAAAAA

09978138.101501

FIGURE 120

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLLFLAFLLLSSRTARSEEDRDGLWDAGWPWSECSRTC GGGASYS LRRLCS
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNPDNPSCLKCQ
AKGTTLVVELAPKVLGDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNCGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVKGPDLHLYLETKTLQGTKGENSELSSTGTFL
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFPCS
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDP CPASDGYQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRVSCVEEDIQGHVTSVEWKCMYTPKMPIAQPCNI
FDCPKWLAQEWSPTCTVTCGQLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK
EKLPVEAKLPWFKQAQELEEAAVSEEPS

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

FIGURE 122

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE
LLRLGARVIMGCRDRARAEEAAGQLRRELQAEECGPEPGVSGVGELIVRELDLASLRSVRA
FCQEMLQEEPRLDVLIINAGIFQCPYMKTEDGFEMQFGVNHLGHFLLTNLLGLLKSSAPSR
IVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSLANILFTRELARRLEGNTNVTNVNLHPG
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE
LLPKAMDESVARKLWDISEVMVGLLK

Important features:

Signal peptide:

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

FIGURE 123

GGGGATTGTAAAGAGGAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTT
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT
TGAAGAAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG
TTACTGAAAAATTATTTTGGGATAAGAGAATTCAGCAAAGATGTTTTAAATATATATAGT
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAATAATTATAACTGGGCA
AGCATGGATGACATATTAATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGT
TGTGTGGAATTATCTGCCTGGCTT

09978388-101501

29

FIGURE 125

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46927, pI: 5.21, NX(S/T): 0
MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQ
MLHPIFEEASDVKEEFNENQVVFARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMKEYR
GQRSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKSDNYRVFERVANILH
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREI
TFENGEEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLH
IQKTPADCPVIAIDSPFRHMYVFGDFKDVLPGLKQFVFDLHSGKLHREFHHGPDPTDTAPG
EQAQDVASSPPESFQKLAPSEYRYTLLRDRDEL

Important features:

Signal peptide:

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

FIGURE 126

ATTAAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCCTCAAATTGTTTCGTAATG
GGATGATGATGAAGAGAGAATACAGGGGTGAGCGATCAGTGAAAGCATTGGCAGATTA

09978188-101501

AGAGGCCCTCTCTGGAAGTTGTCCCGGGTGTTGCGCCGNGGAGCCCGGGTCCAGAGGACNAGG
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTGCGCTCCCGAGCCCAGCCCTTCTTAACCC
AACCCAACTAGCCNCTCCAGCGCCAGCGCCTGTCCCTGTCNCGGANCCAGCGTNACC
ATGCATCCTGCGCTCTTCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC
TTGGGTTTTTACTCCTGTAACAACTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTATGCTGACTGTTGTCGTTTCAGTCAG
ATGTGGCATCCAATTTTGTAGGANGCTTCGATGTCATTAAAGGAAGAATTTCCAAATGAAAA
TCAAGTAGTGTGTGCCAGAGTTGATTGTGATCAGCACTCTGCATAGCCCAGAGATACAGGA
TAAGCAAATACCAACCTTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG
GGTCAGCGATCAGTGAAGACATTGGCAGATTACATCAGGC

FIGURE 128

GCCCACGCGTCCGATGGCGTTACGTTTCGCGGCCCTTCTGCTACATGCTGGCGCTGCTGCTCA
CTGCCGCGCTCATCTTCTTCGCCATTTTGGCACATTATAGCATTGATGAGCTGAAGACTGAT
TACAAGAATCCTATAGACCAGTGTAATACCCGTAATCCCCCTTGTA TCTCCAGAGTACCTCAT
CCACGCTTCTCTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA
TGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCAGGA
CTCTATGACCCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTGAGAAGGAAGGATG
GTGCAAAATTAGCTTTTTTATCTTCTAGCATTTTTTTACTACCTATATGGCATGATCTATGTTT
TGGTGAGCTCTTAGAACAACACAGAGAATTTGGTCCAGTTAAGTGCATGCAAAAAGCCAC
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTTGCTTGTGGAAGACTG
TTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAAATTAATATAAAAT
GATTACCTCTGGTGTGACAGGTTTGAACCTGCACCTCTTAAGGAACAGCCATAATCCTCTG
AATGATGCATTAATTACTGACTGTCCCTAGTACATTGGAAGCTTTTGTTTATAGGAACTTGTA
GGGCTCATTTTGGTTTCATTGAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAAAGTTCATGGGTTTCCTCATCTGTC
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGCTT
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA
TATACTTGCTTTAATCTTAAGCATAAGTAAACATGATATAAAAAATATATGCTGAATTACTT
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAG
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG
TACTACAGATTTTCAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTTCTTTAGT
GCAATACAATAAAACTCTGAAATTAAGACTC

09978168.101501

FIGURE 129

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330
<subunit 1 of 1, 144 aa, 1 stop
<MW: 16699, pI: 5.60, NX(S/T): 0
MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF
CVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLA
FYLLAFFYYLYGMIYVLVSS

Important features:

Signal peptide:

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

FIGURE 130

ATTATAGCATTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCTG
AATCCCCCTTGTA TCTCCAGAGTACCTCATCCACGCTTTC TCTGTGTCATGTTTCTTTGTGC
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCTCTTGGCATATCATATTTGGAGGTATA
TGAGTAGACCAGTGATGAGTGGCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTT
TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACACACACAGAAGAATT
GGTCCAGTTAAGTG CATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

00073135.101501

FIGURE 131

CGGACGCGTGGGGGAAACCCCTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG
GAACAAGATGCGCGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGC
TGTGCTGCTGACCATGGCCTTGGCCGGAGGTTGCGGGACCGCTTCGGCTAAGCATTGTGAC
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTGAGTTGACCTACCCCTTGACAC
CTACCCTAAGGAAGAGAGTGTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTC
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA
GAAGCATATTTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC
ATTCGCTGAACCTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAATGCACCTACTCTTTC
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC
TCTTCATGGACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCC
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA
GCAAAATGTCTTATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTCTTGAAGATGGA
GAAAGTGATGGCTTTTAAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACTCT
TGTCTCTCGGTGATGGTATTGCTTTGGATTGTTGTGCAACTGTTGCTACAGCTGTGGAGC
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG
CTAAACAGATATCCAGCTTCTTCTCTTGTGGTTGTTAGATCTAAAACCTGAAGATCATGAAGA
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTTCTTTT
AAAAGACAAGTGTAATAGACATCTAAAATTCACCTCCTCATAGAGCTTTTAAAAATGGTTTCA
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGS LWVRTQLGLPPLLLLTMALAGSGTASAEAFDSVLGDTASCHRA CQLTYPLHTYP
KEEELYACQRGCR LFSICQFVDDGIDLNR TKLECESACTEAYSQSDEQYACHLGCQNQLPFA
ELRQEQLMSLMPKMHLLFPLTLVRSFWS DMMDSAQSFITSSWTFYLQADDGKIVIFQSKPEI
QYAPHLEQEPTNLRESSLSKMSY LQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTTLVL
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG
PLPTKVNLAHSEI

Important features:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site.

amino acids 90-93

0078188-01501
10511-8818760

FIGURE 133

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCACACCTACCC
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAAATCAGCTGCCATTTCGC
TGAAGTGAAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAA
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

09978388.103501

FIGURE 134

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC
CCAAC TG GGGCTCCCGCGCTGCTGCTGCTGACCATGGCCTTGCCCGGAGGTTGGGGACCG
CTTCGGCTGAAGCATTTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG
TTGACCTACCCCTTGACACCTACCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG
CAGGCTGTTTTCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG
AATGTGAATCTGCATGTACAGAAGCATATTCCTAATCTGATGAGCAATATGCTTGCCATCTT
GGTTGCCAGAATCAGCTGCCATTGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCC
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT
CCGC

09978188.101501

FIGURE 135

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCGGAGGT
GGGGCGCCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCGCGACCGAGC
GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGAGCTGCAATGGGCCGCGGCTG
GGGATTCTTGTTTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC
AGCCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGTTACTTGGATGATTGT
ACCTGTGATGTTGAAACCATTGATAGATTTAATACTACAGGCTTTTCCCAAGACTACAAAA
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCTTTCT
GGAATGACATCAGCCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA
GTTCTGTATGGAATTAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAAAGCTCTGTGAAGCTGATGAC
ATTAGTCCCCTGAAGCTGAATATGTAGATTTGCTTCTTAATCCTGAGCGCTACACTGGTTA
CAAGGGACAGATGCTTGGAAAATATGGAATGTCATCTACGAAGAAAAGCTGTTTAAAGCCAC
AGACAATTAAAGAGCCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAGTGAAGAGAACACT
TTTACAGTTGGCTAGAAAGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGG
CCTACATGCAAGCATTAAATGTGCATTTGAGTGAAGATATCTTTTACAAGAGACCTGGTTAG
AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTTGATGGAATTTTGACTGAA
GGAGAAGGTCGAAGAAGGCTTAAGAACTTGATTTTCTCTACTTAATAGAAGTAAAGGGCTTT
ATCCAAAGTGTTACCAATCTTCGAGCGCCAGATTTCAACTCTTTACTGGAATAAAATTC
AGGATGAGGAAAACAAATGTACTTCTGGAATACTTCAATGAATCAAGTCATTTCCTTTG
CATTTTGATGAGAATTCATTTTTTGTCTGGGGATAAAAAAGAACACACAAACTAAAGGAGGA
CTTTCGACTGCAATTTAGAAATATTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC
GTCTGTGGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG
AAATTGATAGCAAATATGCCAGAAAGTGGACCTAGTTATGAATTCATCTAACCAGACAAGA
AATAGTATCATTATTCACAGCATTGGAAGAATTTCTACAAGTGTGAAAGAATTAGAAAACT
TCAGGAAGTGTGTTACAGAATATTCATTAAAGAAAAACAAGCTGATATGTGCTGTTTCTGGAC
AATGGAGGCGAAAGATGGAAATTTCAATCAAAGGCATAATAGCAATGACAGCTTAAGCCAA
ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATTGTTTTAAGTAAACACATTTT
AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAGTAATACTTTAATAATGTG
GTACAAATTTTAAAGTTAATATTGAATAAAAGGAGGATTATCAAATTAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

0997818-101501

0973788 in 2011

<subunit 1 of 1, 468 aa, 1 stop

MGRGWGFLFGLLGAUVLLSSGHGEEQPPEAAQRFCQVSGYLDCTCDVETIDRFNNYRLF
PRLQKLLSESDYFRYYKVNLRCPFWNDISQCGRRDCAVKPCQSDVPDGIKSAGYKYSEEA
NNLIEECEQAERLGAVDSELSSEETQKAVLQWTKHDDSSDNFCEADIQSPAEYVDLLLNPE
RYTGKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASQGTSEENTFYSWLEGLCVEKRAFY
RLISGLHASINVHLSARYLLQETWLEKKWGHNNITEFQQRFDGILTEGEGPRLKNLYFLYL I
ELRLASKVLPPFFERPDQFLTGNIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH
KLLEDRLHLFRNISIMDCVGCFKRLWGLKLTQGLGTALKILFSEKLIANMPSEGPSYEFH
LTROEIVSLFNAFGRISITSVKLELNFRLNLONTH

Signal peptide:

amino acids 1-23

amino acids 280-283 and 384-387

amino acids 94-97

amino acids 20-23 and 223-226

amino acids 216-222

amino acids 338-343

FIGURE 137

GCTGGAAATATGGATGTCATCTACGAGAAACTGTTTTAAGCCACAGACAATTAAAAGACCTT
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTTACAGTTGGCTAGAA
GGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA
ACATTACAGAATTTNAACAGCGATTTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG
CTTAAGAACTTGATTTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCAT
CTTNGAGCGCCAGATTTTCAACTNNTTACTGGAAATAAAATTCAGGATGAGGNAAACAAAA
TGTTACTTTTGGAATACTTCATGAAATCAAGTCATTTCTTTGCATTTTGATGAGAATTCA
TTTTTTTGCTG

09978188-10504

FIGURE 138

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTTGGGAGGGGGCAGGATGGGAGGGAA
AGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC
CGATCAGGCATATGGAACTCCCCITCGTCACTCACCTGTTCTTGCCCCCTGGTGTCTCTGACAGG
TCTCTGCTCCCCCTTTAACTGGATGAACATCACCCACGCCATTATCCAGGGCCACCAGAAG
CTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC
GCCCCCTGGGATGGGCCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGG
GGCCCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTTCATCTC
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGTAGGGGGATTTC
ATGGTGAGCTAAGGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAGAGAA
GTGTGGTAAGGGAAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCTAGAAAAGCAAA
AGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT
GCCCTCCCAAGCCTGGGAGTAACATATTTCCCCCATCCCCAGGCCTGTGCCCCCTCTCTGGTCT
CGTGCTTGTGGCAGCTCTGTCITCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCA
GCCTCAGGGAAGCCTGGCACCCACTGCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTT
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCCTGGCAAAGGG
CCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAGCTCCATGTTTCCTAACAGA
TTCAGACTCCTGGCCAGGTGTGGTGGCCCCACCTGTAAATTCTAGCACTTTGGGAGGCCAAG
GTGGGCAGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACTCCAT
CTCTACTAAAAAATAAATAACAAAAATTAGCTGGGTGCGCTAGTGCATGCCTGTAATCTC
ATCTACTCGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG
AGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAAA
AATAATAATAATAATAATTACAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGAG
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

09970136.10501

FIGURE 139

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039
><subunit 1 of 1, 124 aa, 1 stop
><MW: 13352, pI: 5.99, NX(S/T): 1
MELPFVTHLFLPLVFLTGLCSPFNLDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW
DGPSGDRRGDVYRCFVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGFMVS

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

097018-10154
T0101-9818/660

FIGURE 140

CACAGTTCCCACCATCACTNTCCCATTCCTTCCAACTTTATTTTTAGCTTGCCATTGGGA
GGGGGCAGGATGGGAGGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC
TTCTCATACTGGACAGAAACCGATCAGGCATGGAAC TCCCTTCGTCACTCACCTGTTCTTG
CCCCTGGTGTTCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT
ATTCCCAGGGCCACCAGAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGAGGGGGGACGTT
TATCGCTGCCCTGTAGGGGGGGCCCCACAATGCCCATGTGCCAAGGGCCACTTAGGTGACTA
CCAACTGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGA
CAGATGGTGATGG

105101-8782660

FIGURE 141

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCGGGCTCTAGAACA
ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTTCTGAAGAAAGATGGCT
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
ACGCATTGATTCATGTTTGCTCAAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAAGTGATCGCGCCTGGAGA
AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATC
ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCAGACACTCAGCCTG
GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTTGAGTTC
CTTGTTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAAACATGTCAAAATGGTGAGGAGTGG
GGGTATTCAGTGCACTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
CATTGCTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCCTTTGTTGGCTTCATGCTGATCCCTTGT
GGTCTGCCACTGTTCTGCTCTGGAATAAGGGCCGGCTGCTCCAGTACTCCTTTGCCCCGTGG
TGGTCTCCAGACACCTTGAAAAATAACCAATTACCCCCAGAAGTTAATCAGCTGCAGAAGG
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCCTGAGGAACTCCTCAGGGCCTGGAT
CTCATAGGTTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACC
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
GCCTGTGTCTCAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTTGTCTAACAGAAAC
TGACTGAGGCTTAGGGGATGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC
CTGGGAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC
TACACACCTGCTAAACACACACACAGAGTCTCTCTCTATATATACACAGTACACATAAA
TACCCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTAG
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
GGCTTGGAGAGCCCACTTTCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
TGTTGAGTTCACTTCAAGCCCAATGCCGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
AGGTGACCTGGAGGAAGGTACAGCCCACTGAAAATGGGATGTGCATGAACACGGAGGATC
CATGAATCTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGAGGTGAAATGTATGT
GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTGTTGTGCTCCTTTTTTC
TGTTGGTAAAGTACAGAATTCAGCAAATAAAAGGGCCACCTTGGCCAAAAGCGGTAAAAAA
AAAAAAAAA

09978188.104501

FIGURE 142

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033

<subunit 1 of 1, 311 aa, 1 stop

<MW: 35076, pI: 5.04, NX(S/T): 2

MQTFMTMLEEIIWTSLFMFFYALIPCLLTDEVAILPAPQNL SVLSTNMKHL LMWSPVIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSL TEGPECDVTDITATVPYNLRVRATLGSQTS AW
SILKHPFN RNSTILTRPGMEITK DGFHLVIELEDLGPQFEFLVAYWRREP GAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECV EVQGEAIPLV LALFAFVGFM LILV
VVPLFVWKMGRL LQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation site.

amino acids 40-43 and 134-137

Tissue factor proteins.

amino acids 92-119

Integrins alpha chain proteins

amino acids 232-262

007812 8218260

FIGURE 143

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTGAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCAGATGAAGTGGCCATTCTGC
CTGCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAAAGTGTACTATTCTGTGGAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACCTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTGAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGCGCCTANTGGAGGAGGGGCGAACCCTTGCGGCGCAAGGG
GTTCGCAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGGTTGAT

0097516-10501

FIGURE 144

CCCACGCGTCCGCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAGGAGAGAGGGAGGAGGAG
GAGGAGATCGGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC
GGAGAGGAGGTGTGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA
GTAGGAAGATCAGGAGCTAGAGGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAAGAGG
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG
GCTGCTTTGGCATTTGGGGAACCTGGGACTCCCTGTGGGGAGGAGAGGAAAAGCTGGAAGTCTT
GGAGGGACAGGGTCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGCAGGGCGTTGGG
CAGGGGTCCCTCGGAGGCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCCTCGAGC
GCTGGTACTCTGGGCTGCAGTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG
ACTGGTGGAGCTACAAGGATAATCTCCAGGAAACTTCGTGCCAGGGCCTCCTTTCTGGGGC
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCATTAAGGCTCAGCACTGGAGGAGAGA
AGCTCCGGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCTGCTGCAACCCGACCT
GTGGTCAATGTGTCTGGAGGTCCCTCCTTTACAGCCACCGAATCAGTGAAGTGCAGGCTGCT
GTTTGGAGCTCGCGACGAGCCGGCTCGGAACATCAGATCAACCACGAGGCTTCTCTGCTG
AGGTGCAGCTCATTCACTTCAACCAGGAACTCTACGGGAATTTACGCGCTGCCTCCCGCGGC
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCATTCTC
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCTACAAGAATGATGCCTACTTTC
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACTATCAGGGC
TCTCTCAGACCCCGCCTGCTCCGAGACTGTACCTGGATCCTCATGACCGGGCCCTCAA
TATCACTCTCCCTTCAGATGCATCTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT
TCCAGAGCCTCAGCGGTAACAGCCGGCCCTGCAGCCCTTGGCCCACAGGGCACTGAGGGGC
AACAGGGACCCCCGGCACCCGAGAGGCGCTGCCAGGCCCCAACTACCGCCTGCATGTGGA
TGGTGTCCCCATGGTCTGAGACTCCCTTCGAGGATTGCACCCGCCGCTCTAAGCCTC
CCCACAAGCGGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGACAGAATACTTA

0975138.10501

09078168 = 121501

<subunit 1 of 1, 328 aa, 1 stop

MGAAARLSAPRALVLWAAALGAAAHIGPAPDPEDWWSYKDNLCQNFVGPFPFVGLVNAAWSLC
AVGKRQSEVVDVELKRVLYDPFLPPLRLSTGGEKLRGTYLNTGRHVSFLPAPRPVVNVVSGGPL
LYSHRLSELRLFLGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL
FVNVASTSNPFLSRLLRNDRITIRISYKNDAYFLQDLSLELLFPESFGFITTYQGSLSLTPPCSE
TWTWILIDLRLNTHVPSLQMHSLRLLSQNPFSQIFQSLSGNSRPLQPLAHLRGNRDRPHRPER
RCVGPNRYLRNDVGSVPHR

Signal peptide:

amino acids 1-23

amino acids 177-199

amino acids 118-121, 170-173 and 260-263

amino acids 222-270, 128-164 and 45-92

FIGURE 146

GGCGCTGGTTCTGCGGTACTGGCTGTACGGAGCAGGAGCAAGAGGTGCGCGGCCAGCTCCGCCGCCGAGCCTC
 GTTGGTGTCCCGCCCTCGTCTGCTCCCTGTCAGCTACTGCTCAGAAACGCTGGGCGCCACCCTTGGCAGACTTAACGAA
 GCAGCTCCCTCCCAACCCACATGTCAGGTCTAATTTTGGACGCTTTGGCTGCCATTTCTTCCAGGTTGAGGGAGC
 GCGAGAGCGGAGGCTCGCGTATTCTCGAGTCAGCACCCACGTCGCCCCGGAGCGCTCGTGCTCAGGCCCTTC
 GCGAGCGGGGCTCTCCGCTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCGAGAGCGCGGCGCTCGGTTTGGCT
 CACCTCTCCCGAGAACTTCCACATGGAGAGCCAAAGAGGTGGAAGAGCCTGTCTTGGAGATTCTTCTGGGGAA
 ATCCTGAGGTCAITTCATTATGAAGGTGTAACGCGCGGGAGTGGCTCAGAGTAAACCAGTGGCTGTTCATGGCTAGA
 GCAATTCAGCCCATGGTGGTTCCCAATGCCACTTTATTGGAGAACTTTGGAAAAATACATGGATGAGGATGGT
 GAGTGGTGGATAGCCAAACACAGAGGAAAGGGCCATCAGACAAATGACATGACAGATATTTTGGACCTTCAT
 AATAAATTCAGAACTCAGGTGTATCCAAACGCTCTAATATGGAGTATATGACATGGGATAGAGCTGGAAAGA
 TCTGCAGAACTCTGGGCTGAAAGTTGCTTGTGGAAACATGGACCTGCAAGCTGTTCATCAATTGGACAGAAT
 TTGGAGACACATGGGGAAGATATAGGCCCGGACGTTTCATGTAACATCGTGGTATGATGAAGTGAAGACCTT
 AGCTACCCATATGAACATGAATGCAACCCATATTTGCCATTGAGGTGTTCTGGCCCTGTATGTACACATTATACA
 CAGGTCTGTGGGCAACTAGTAACAGAATCGGTTGTGCCATTAAATTTGTGTACATAACATGAACATCTGGGGGCG
 ATATGGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCAAAGGGAACCTGGTGGGGCCATGCCCTTACAAA
 CATGGGCGGCCCTGTCTGCTTGCCACCTAGTTTGGAGGGGGCTGTAGAGAAAAATCTGTGCTACAAAGAGGG
 TCAGACAGGTATTATCCCCCTCGAGAGAGGAAACAAATGAAATAGAACGACAGCAGTCACAAGTCCATGACACC
 CATGTCGGGACAAAGATCAGATGATAGTAGCAGAAATGAAGTCAATAGCGCACAGCAAAATGTCCCAAATTTGTTCT
 TGTGAAGTAAAGATTAAAGAGATCAGTGCAAGGAAACAACTGCAATAGGTACGAATGTCTGCTGGCTGTGTGGAT
 AGTAAAGCTAAAGTTATTGGCAGTGTACATTTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT
 ATAATAGACAAATGATGGTGGCTGGGTAGATATCCTAGACAGGAAGAAGCAATTTTTCATCAAGTCCATATAG
 AATGGTATTCAAACTTTGGCAAAATATCAGTCTGCTAATTCCTTCAAGTCTCAAAAGTAAACAGTTCCAGGCTGTG
 ACTGTGGAACCACTGTGGAAACAGCTCTGTCCATTTCTAAGGCTGCTTACATGGCCCAAGATGATCTGTCTC
 CGTAACTGTATGCAAGCAAACTCAGATTATGCTCGTGTAAATGGAACTCGAGTTTATCTGATCTGTCCAGTATG
 GCCCTCAGAAATCATGTGATCTGGAGTGGTTCGAAATCAGCGTGGTTATGTTGATGTAAATGCTGTGACAAAGA
 AAGACTACATTTGCTTCTTTTCAGAAATGGAATCTTCTCAGAAAGTTTACAGAAATCTCCAGGAGGAAGGCATTC
 AGAGTGTGCTGTGCTGTAAGTAACTCTGGAAGAGGACCATAAGACTATTCCAAATGCAATATTTCTGA
 ATTTTGTATAAACTGTAACTACTGATGTACAGAGTACATCAACTATTTTCAGCCCAAAAGAGGTGCCAAATGCATA
 TAAATCTTGATAAAACAAAGCTATATAAATAAAACATGGGACATTAGCTTTGGGAAAAAGTAATGAAAAATATAATGG
 TTTTAGAAATCTGTTGTTAAATATTGCTATATTTCTTAGCAGTTATTTCTACAGTTAATTACATAGTCATGATT
 GTTCTAGCTTTCATATATTATATGTTGCTTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAAT
 GCCCTCAGAAATCATGTGTCATTTAAAAATAATCGACTTAAAACTGAAAGAAACCTTATCACTTTTCCCC
 AGTTCATGCTATGCCATTACCACTCCAAATAATCTCAAATAATTTTCCACTTAATAACTGTAAAGTTTTTTTC
 GTTAATTTAGGCGATATAGAATAATTAATCTGATATTGCACTTCTATTTTATATAAAATAATCTTTAATATC
 CAATGAATCTGTTTAAAAATGTTTGAATTCCTTGGGAATGGCTTAAAAATAAATGTATAAAGTCAGAGTGGTGGT
 ATGAAACACTTCCTAGTGATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTTCTATGTACTGTTA
 AAATTGAGGTACATATTTTCTTTTGTATCTGGCAAAATCTCCTGCAAGCCAGGAGATATAATAGCAAAAGTT
 GAACAAAGATGAACATAATGTTATACATTACCATTTGCCACTGATTTTTTAAATGGTAAATGACCTTTGATATAA
 ATATTGCCATATCATGGTACCTATATAATGGTGTATATTTGTTCTATGAAAAATGATTTGTGCTTTGATACATAA
 AATCTGTAAAAATTTAGTTTTCGGTAAATTTTTTTCTGCTGGTGATTTACATATAAATTTTTCTGCTGGTGGGA
 TAAACATTAATAATTAATCATGTTTCAAAAAAATAA

09978198.101501

FIGURE 147

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417
<subunit 1 of 1, 500 aa, 1 stop
<MW: 56888, pI: 8.53, NX(S/T): 2
MKCTAREWLRVTTVLFMARAI PAMVVPNATLLEKLLLEKYMDEDGEWWIAKQRGKRAITDNDM
QSILDLHNKLRSQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW
GRYRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFFRCSGPVCVTHYTVVWATSNRIGCAINLC
HNMNIWGQIWPKAVYLVLCNYSKGNWGWGHAPYKHGRPCSA CPSPFSGGCRENL CYKEGSDRY
YPPREETNEIERQQSQVVDTHVTRSDSSRNEVIS AQQMSQIVSCEVRLRDQCKGTTTCNR
YECFAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKHYFIKSNRNGI
QTIGKYQSANSFTVSKVTQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIG
TRVYDLSSICRAAVHAGVVRNHGGYVDVMPVDKRTYIASFQNGIFSESLQNPPGGKAFRV
FAVV

Important features:

Signal peptide:

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

0978133 10450
105017 89182680

THE UNITED STATES OF AMERICA

[illegible]

FIGURE 149

MSLLPRRAPPVSMRLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNANNEKRRVYEE

Signal sequence:

amino acids 1-34

005101-8818/660

FIGURE 150

GCCCCAGGGACTGCTATGGCTTCCTTTGTTGTTCAACCCGGTCTGCGTCA~~at~~GTAAACTCCAATGTCCTCCTGTG
 GTTAACATGCTCTTGCCATCAAGTTCACCCCTCATTGACAGCCAAAGCAGATATCCAGTTGTCAACACAAATATATGG
 CAAAATCCGGGGCCTAAGAACACCGTTACCCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCCAT
 TGCCTCACCCCCCACTGGAGAGAGGGCGGTTTCAGCCCCAGAACCCCGTCTCTCTGGACTGGCATCCGAAATAC
 TACTCAGTTTGTCTCTCTGTGTGCCACAGCACCTGGATGAGAGATCTTACTGCTGACATGTGCCCATCTCGGTT
 TACCGCCAAATTTGGATACCTTGTGATGACCTATGTTCAAGATCAAAATGAAGACTGCCTTTACTTAACACTCTACGT
 GCCACCGGAGATGTGAGCCCAACACAAAGAAAAACGCAAGATGATTAACGAGTAATGACCGGTGTGAAGACGGA
 TATTCATGATCAGAACAGTAAGAAGCCCGTCTATGGTCTATATCCATGGGGGATCTTACATGGAGGGCACCGGCA
 CATGATTACGGCGAGCATTTTGGCAAGCTACGGAACGCTATCGTGATCAACATACTAACCTACCGTCTGGGAATACT
 AGGGTTTAAAGTACCGGTGACAGGGCAGCAAAAGGCAACTATGGGCTCTGGATCAGATCAAGACCTGCGGGT
 GTGTGAGGAGAAATGTGGAGCCTTTGCGGGGACCCCAAGAGATGACCTATTTGGCTCGGGGGTCTGGGGCTCT
 CTGTGTGAGCCTGTGACCCCTGCCACTACTCAGAAAGGTCTCTTCAGAAAGGCATCATTCAGAGCGGACCGC
 CCTGTCCAGCTGGGCACTGAACACAGCCCGGCAAGTACACTCGGATATTGGCAGACAAAGGTGGCTGCAACAT
 GCTGGACACACGACATGGTGAATGCTGCGGAACAAAGACTACAAAGGAGCTCATTCAGCAGACCATCAACCC
 GGCCACTTACCACATAGCCTTCGGGCGGTGATCGACGGCGAGCTCATCCAGACGACCCCCAGATCTTGTATGGA
 GCAAGGCGAGTTCTCTCACTACGACATCATGCTGGGCGTCAACCAAGGGGAAGGCTGAAGTTCTGTGGAGCGCAT
 CGTGGATAACGAGGACGGTGTGAGCGCCCAACGACTTTGACTCTTCCTGTCCAACCTCGTGGAACACTTTAAGG
 CTACCTGTAAGGAGAAAGACACTTTTGGCGGAGACTATCAAGTTTCATGTACACAGACTGGGCCGATAAGGAAACCC
 GGAGACGCGCGGAGAAACCTCGGTGCTCTCTTTACTGACCAAGTGGGTGGCCCCCGCGTGGCGCGCAAGCT
 GCACGCGCAGTACGGCTCCCCACCTACTCTTATGCTCTTCAGCTCCCATGATCGGTCCCAAGAGCTCTTCAG
 TGTAACTTTCCAAAGAACGATCGTATGCTCAGCGCGGTGATGACCTATGGAGAACTTCCGCAAACTGG
 TGATCCAAATCAACGAGTCTCTCAGGATACCAAGTTTCATTACACAAACCCCAACCGCTTTGAGAAGATGGCGT
 GTCCAAGTATAATCCCAAGAGCAGCTCTATCTGCATATTGGCTTTGAACCCAGAGTGAGAGATCACTACCGGGC
 AACGAAAGTGGCTTTCTGGTTGGAACCTGTTCTCTCATTTGCACAACTTGAAAGAGATATTCAGTATGTTTCAAC
 AACCAAAAGGTTCTCCACAGACATGACATCATTTCCCTATGGCACCCCGGAGATCTCCCGCAAGATATGGCC
 AACCAACAAAGCCGAGCAATCACTCTGCCAACAATCCCAACACTCTAAGGAGCCCTCACAAACAGGGGCTGA
 GGACACAACTGTCTCATTTGAACCAAGAGATTTATTCACCGAATTAAGTGTCAACATTCGCTCGGGGCGCT
 GCTCTCTCTCTCAACATCTTAGCTTTTGGCGGCTGTACTACAAAAGGACAAAGAGGCGCATGAGACTCAAG
 GCGCCCCAGTCCCCAGAGAAAACCAACAAATGATATGCTCACATCCAGAACGAAGAGATCATGCTCTGAGAT
 GAAGCAGCTGGAAACAGATCAAGAGTGTGAGTGTGCTGAGGCACACGACACTGAGGCTCACTCGCCCGCAGAT
 TACACCTCTCAGCTGCGCGGTGCGCAGATGACATCCACTATGAGCGCAACACCATCAACATGATTCCAAA
 CACACTGACGGGATGAGCCTTTGACACTTTTAAACACTTCAGTGGAGGACAAAACAGTACAAATTTACCCCA
 CGGACATTTCCACCATAGAGTAT~~at~~CTTTGCCCTATTTCCTTCTATCCCTCTGCCCTCACTCCGCTCAGCAACAT
 AGAAGAGGGAGGAAAGAGAGAAAGGAGAGAGAGAAAGAAAGTCTCCAGACCGGAATGTTTGTGCCCACT
 GACTTAAAGCAAAAATGCAAAAAGGCACTCA~~at~~CCATCCCGGAGACCTTATGTTGGTGTGTTTCCAGTATTAC
 AAGATCAACTCTGACCTGTGAAATGTGAGAAGTACAATTTCTGTTAAAAATAAGTCTTTAAGATCTTACCA
 CTCCAATCAATGTTTGTGTGATAGGACATCA~~at~~CAATTCAGGGCCCGGGTGTTCACAGCTCATGGAGCAGCT
 GACACTCTGAAACTCAGCCAGGACACTTGATATTTTAAATTAACATGGAAGTTTAAACATTTCTTTCTGTGC
 CACACATGGATGGCTCTCCTTAAAGTGAAGAAAGATCAATGAGATTTTCCCGCAGCATGGAGCTGTAATCCAG
 AGAGAAGGAAACGTAGAAATTTATTTATTAAGAATGGACTGTGACGCGAATCTGTACGGTTCTGTGCAAGAG
 GTGTTTTCGACGCTGAACATATATTTAAGAGACTTTGT

FIGURE 151

MLNSVLLWLTLALAIKFTLLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP
PTGERRFQPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMLPWFNLTANLDTLMTYVQDQN
EDCLYLNIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFGGDPKR
VTIFGSGAGASCVSLLTLSHYSEGLFQKAIISGTALSSWAVNYQPAKYTRILADKVGCNML
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLG
VNOGEGLEKFDGIVDNEGDVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIKFMYTDWADKENP
ETRRKTLVALFTDHWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKP SWADSAHGDEV
PYVFGIPMIGPTLEFSCNFSKNDVMSAVVMYWTNFAKTGDPNPQVPQDTKFIHTKPNRFE
EVAWSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKV
PPDMTSFPYGTRRSPAKIWPTTKRPAITPANNPKHSDPHKTGPEDTTVLIETKRDY
STELSVTIAVGLASLLFLNLAFALYKKDKRRRHETHRRPSPQRNTTNDIAHIQNEE
IMSLQMKQLEHDECESLQAHDTLRLTCCPPDYTLTLRRSPDDIPLMTPNTITMIPNT
LTGMQLHTFNTFSGGQNSTNLPHGHSTTRV

Signal sequence:

amino acids 1-24

Transmembrane domains:

amino acids 189-204, 675-692

GGGAAGATAGCGCGGCACACTCTGGGACCCCTTGGGTCGTGGCAGCAGTGGCGGCATGTTTGT
CGGCTCGGGATGGGTCCAGGATGTTAATCTCTCTTCTTTCTTTGGGGTCTGGGCGAGGGCCA
CAGCAAGATCGGGGCGGGTCAACCGTTTCGAGTACTTGAACCGGAGCACTCGCTGTCCAGCGC
CTACCAAGGTGTGGGCGCAGGCAGTCTCTCATCTGTGGAATCTGATGGGCAATGCATGGTGA
TGACCAGGTATATCCGCCTTACCACAGATATGCAAAAGTAAACAGGGTGCCTTTGTGAACCGG
GTGCCATGTTTCTGAGAGACTGGGAGTTGCAGGTGCACCTTCAAATCCATGGACAAGGAAA
GAAGAACTCTGCATGGGGATGGCTTGGCACAATCTGTGACAAAGAGTCGGATGCGACCGAGG
CTGTGTTTGGAAACATGGACAAATTTGTGGGGCTGGGAGTATTTGTGACACCTACCCAACT
GAGGAGAAGCAGCAAGAGCGGGATTTCCCTACATCTCAGCCATGGTGTGAACACCGGCTCCCT
CAGCTATGATCATGACGCGGATGGGCGGCTACAGAGCTGGGAGGCTGCACAGCCATTGTTC
GCAATCTTCATTACGACACCTTCCCTGGTGATTGCTACGTCAAGAGGCATTTGACGATAATG
ATGGATATTGATGGCAAGCATGAGTGTGGAGGAGCTGCATTGAAGTCCCGGAGTCGCGCTGCC
CCGGGCTACTACTTCGCGCACTCTCCATCACTGGGGATCTTCAGATAATCATGATGTCA
TTTCTGTGAAGTTTGTGAAGTCAGAGTGGAGAGAACCCCGCAAGAGGAAAAGCTTCATCGA
GATGTGTTCTTGCCCTACGTGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCGCCG
CCTGAGTGGCTGGCCCTCTTCTCATCGTCTTTTCTCCCTGGTGTTTTCTGTATTTGCCA
TAGTCAATGGTATCATATCTTCAACAAGTGGCAGGAAACAGAGCCGATGCTTACTCGA
GCCCTCCTCGCTGCCAACCACTTTGTGACTGTCCACCATGAGGTATGGAAGGAGCAGGCAGT
GCCTAGCATGCGACCTGGAGAGTGTTCTGTCTAGCAGCTGGTTGGGGACATATTTCTG
TCACTGGAGTTTGAATGACGGGAGCCCGCATTCCCATGGTTGTCATGGGGACATCTAACT
CTGGTCTGGGAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCCTTTCCCTGCACTCC
TTCCATGTGGGAGCAGAGGTGTGAAGAAAGTTTACGTGGTGTGATGCAAAAATCAGACA
AGAATTTATAGACCCGAGGTCGCGTGTGTTTGAATCAGAAGGCCCTTCTACTTCAGTTTGT
AATCCACAAGAAGATTAAGAACTGGTAAACACCAACAGGCTTTCTGCAATCCATTCGTTGGGTT
TTGCAATTGTGACCAACCCCTCTGCTACTGAGGAGCTTTCTTTGAAACAGGATGGAAGT
TCTTCCCTGCCTTACCTTCTTTTCACTCCATTATTGTCTCTCTGTGTGCAACCTGAGCTG
GGAAGGCAATTTGGATGCCTCTCTGTGGGCGCTGGGGCTGCAGAACACCTCGGTTTCACT
TGCCCTCATTAGGTGGCCCTAGGAGATAGTCCTTCTGTTTGGATCACTGTTCCATGACAT
GGGTCTGGGTCTATTGGCATCTGATGCTCATGCGCTCCCAATCGAGTCTCTCAGGCCCTCAGT
AAGTTTGGCTTAAAGGTTGGTGTTAAATCAAGAAGAGCTCGAAGCATCATGGATGCCAT
GATTAGCTGTGCAACTGACACAGCTCCAGGTTTGATCAAACCAAAGCAACATTTGTCAATGT
GTCTGACCATGTGGAGATGTTTCTGGAAGCTGTAGAGCTGTAGCTGTGATGTTTGTAGT
TAGCAATTTTGGAAATCCCACTTTGAGTGTGAAGGTGAAGAGAGCTTTCTTCTTACCTTT
GGGTCTGGATATTGGCCAGGAAGAAATTTGGCTTTTCTTCTTAAATGGCAAGAGCAGT
TGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCTTCATCATCTGTGCTGGAAGAGT
CACTGTCAATTTGAGCAGCAGAGCTGAGTCTGCGGCTCTGTCAACCCCTATTTCATCTGCCCTTA
TTTGACAAGGTTACATGCTGCTGCTACTGCTCCCTGGGATTAATCAGTTACAGGCCAG
AGTCTCCTTTGGAGGGCTTGGAACTCTGAGTCTCTATGAACCTCTGAGCTCGAATTAAGAT
TCTTAAATCATCCGATGAGGACCAAAGGAAAAAAGGAGGGCGGCGCAGCTCTAGAGTCTG
ACCTGCATAGGGAATAACCAAGCTAATAAGCTTGGCCGCAATGG

FIGURE 153

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39711, pI: 8.70, NX(S/T): 1
MAATLGPIGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPPQVGAGQTFEYLKREHSLSKPYQ
GVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKIHGQGKKN
LHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDTPNEEKQQQERVFPYISAMVNNGSLSY
DHERDGRPTLGGCTAIVRNLHYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG
YYFGTSSITGDLSDNHDVISLKLFEFTVERTPEEEKLHRDVFLPSVDNMKLPENTAPLPPLS
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY
```

Signal sequence:

amino acids 1-38

Transmembrane domain:

amino acids 310-329

FIGURE 154

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT
 CTGATGTGGTGGTGTCTTAACCTCAGTGGGACTCCAAGATTTCCATGAAGAAAATCAGTTGTCTTCATTCAAGAAAT
 TGGGTGTCTGGCTCAGAATTTCTGCAGCTGGTGAAAAATCTGTTTTCTAGAAAGAGGTTTAATTAATGGCTGCAGTCT
 GACATGTTCCGATTTTGAAGTGAAACCATGAAGAGAAAATAGAAATACTTAATAATGCTTTTCCGCAACCGCTTCT
 TGCTGCTCTGCGCCCTGGCTGCGCTGCTGCTGCTTTGTGAGCCTCAGCCTGAGCTTTCTCCACAGTTCTTCCACCTGATCCCGGTGT
 CGACTCTAAGAATGGATGAGTAGCAAGAGTCGAAAGAGAATCATGCCCCGACCTGTGACGGAGCCCCCTGTGA
 CAGACCCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCGAGTGTGGCCGAGCGCAGCATGGAGAGTCAATGCC
 CGCATCATTTTAAAGCTGGTCTCAGTGCATGTGTTTCATTGCGCACGGAGACAGGTATCCCACTGTATGTTCATCCCA
 AAACAAGCGCAGCAAAATTTGACTGCTCCTGCTGGCTAAACAGGAACCGTATCACCCAAAATGGAAGCTTTCA
 TTAGTTCACATGTCAAAGGATCCGGAGCCTCTTTGAAAGCCCCCTGAACTCTTGTGCTCTTTACCCAAATCACC
 CATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGACAGCATTTCAGAAACGGTCAGCTGTGAGGGATA
 TCTATCTAAAGAAACAACAACCTCTGCCCCAATGATGTGTCTGCAGACAGCTCATTTAGAGACCATGGGAAAA
 GCCCGACCCCTACAAAGTGGCTGGCTTCTGCTTTATGGCTTTCTCCAGATTTTGACTGGAAGAAGATTATTTC
 GGCACCAAGCAAGTGCCTGTCTGCTCTGGAAGCTGCTATTGCCCGGTAAAGAAACAGTATCTGGAAGAGGAGC
 AGCGTCTGTCAGTACCTCTACGTTTGA AAAACAGCCAGCTGGAGAAGACCTACGGGAGATGGCCAAAGATCGTGG
 ATGTCTCCCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTCTGCCCAATGTGAGT
 TTCCCTGTACCAAGAAATGGCTGTGTTGACATGGAGCATTCAAGGTAAATGAAGCCCATCAGATCGAGGATGAAA
 GGGAAAGACGGGAGAAAGAAATTTGACTTCGGGTATTCTCTCTGGGTGCCACCCCATCTGAAACCAACCATCG
 GCCGGATGCAGCGTGCCACCGAGGGCAGGAAGAAGAGCTCTTTGCCCTCTACTCTGCTCATGTGTCACTCTGT
 CACCAGTTCTCAGTGCTTTGGGCTTTTTCAGAACCAAGTTCCCAAGTTTTCAGCCAGGTTGATCTTTGAGCTTT
 GGCAAGA CAGAGAAAAGCCAGTGAAACATTCCGTCGGGATTCTTTCAATGGCGTATGATGTACATCTCACACCT
 CTTTCTGCCAAGACCACCAAGCGTTCTCCCAAGCCCATGTGCCCGCTGAAAACCTTGGTCCGCTTTGTGAAA
 GGGACATGTTTGTAGCCCTGGGTGGCAGTGGTACAAATTAATGATGATGATGTCAGGGAAGGATTCTAAAGG
 TATGAGTACAGCAGTATAGAAATCCATGCCAATACAGAGCATAGGGAAGGTCCACTTCAGTTTGTCTGTGTAC
 TAAGGGTAGAAGATTATGCTTTTAAAGGCTAAATATTGTTGTGGGAACACAGATGGTTGGGGTTGAACAGT
 AAGCACATTTGCTGCAATGTGGTACGTGAATGTCTGTGTACAAAATGGCCAGTTTCAGAGGAATAGAGAGTACTT
 TATCATAGAGCTCTGCTTTAGAATGCGCAGAATAATATAGTTCAAGACCTGAAAGTTGCCAATCCAAGTTTGCAC
 TCTTCTGGCTGCCCATGTGTACTATGTGATGGAACCCAGCACACCTCAACCAAAATTTTAAATCTTAGACATT
 TTTCTGCTGCTGCTTGAAGATTTCTGTGAAGTGATTTATCTAAAATAAGGTTTGGCAAACTTTTCTGTGAAGG
 GCCAGATTTGAAATATTTTCAGCTGTGTGGACCAAAAGGCCACATACAGTCTCTGTGATACCTACTCAACTCTGT
 TTCTGAAGCAGGAAGCCACCAACAGCAGTACATAAAGGAATATGTGTAGCTGGGTTCGCCAGGCAGACAAACA
 GATGGTCAACAGACTTGGCCCTGGGCTGTAGTTTGTGACCCCTCATCTAAAAAATAGGCTATACTACAATTGC
 ACTTCAGCACTTTGAGAACGGTGTGAATACCAAGAATTATCAATGGTCTCCTCCAGTAACCTCTGTGAGAAACA
 CAGAATTTTGGTCTGTATCTGCACACTAGAACAAAACCTTGAGGGTAAATAAACATTGAATTAGAATGAATCATAGAA
 AACTGATTAGAAGAAATCTGTGATGTTTATGATGATTGTGGTACAAGATAGTTTAAAGTATGTTCTAAATATTGTT
 CTCTGTAGTCTATTTTTCTGTATATGCTGAAATTTTGTATGCCATTAGTATTTTATAGTTTGAAGAAAATATT
 TTCTAAGACCAAGTTTAGATGACTCTTATCCCTGTAGTAATATTCAATTTGCTGTACCTGCTGGTGGTTAGAAG
 GAGGCTAGAAGATGAATTCAGGCATTTCTTCCAATAAACTAATTATGGCTCATTCCCTTTGACAGCTGTAGA
 ACTGGATTCAATTTTAAACCATTTTCATCAGTTTCAAAATGGTAAATCTGATGATTTTTAAATGCGTTTTTGA
 AGAATTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATATTAGAAGCAATTATAATTACATCTG
 TGATTTCTGAACATATGGTGCTAATTCAGAGAAATGGAAGGTGAAAGTGAGATTCTCTGTGTGTCATCGGCATTCC
 AACTTTTCTCTTTGTTTGTCCAGTGTGCAATTTGAATATGCTGTTCTATAAAATAAATTTTAAAGATAA

09978182 101501

FIGURE 155

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329

><subunit 1 of 1, 480 aa, 1 stop

><MW: 55240, pI: 9.30, NX(S/T): 2

MLFRNRFLLLLALAAALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDVPVTEPPVTDVPVY
EALLYCNIPSPAERSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKP
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGCVVQHLQNGQLLRDIYVK
KHKL LPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSM LCHFCHNVSFPC
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELF
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSHSVRILYNGVDVTFHTSF
CQDHHKRSPPKPMCPLENLVRFVKRDMFVALGGSGTNYDACHREGF

Signal sequence:

amino acids 1-18

2019年10月10日

[illegible]

FIGURE 157

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306

><subunit 1 of 1, 916 aa, 1 stop

><MW: 100204, pI: 4.92, NX(S/T): 4

MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVPPELEKGSRVGDISRDLGLEPRELAER
GVRIIPRGR TQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVVEVEVR
DINDNAPYFRESELEIKISENAATEMRFP LPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA
DGSKYPELV LKRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVL DANDNAPAFAPQPEYR
ASVPENLALGTQLLVVNATDPDEGVNAEVRYSFRYVDDKAAQVFKLDCNSGTISTIGELDHE
ESGFYQMEVQAMD NAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLNVN
DQDSEENGQVICFIQGNLPFKLEKSYGNYSLVTDIVLDREQVPSYNITVTATDRGTPPLST
ETHISLNVADTNDNPPVFPQASYSAYIPENNPRGVSLSVSTAHDPCENNAQITYSLAENTI
QGASLSSSYVSINSDTGVLYALSSFDYEQFRDLQVKVMARDNGHPPLSSNVSLSLFVLVDQNDN
APEILYPALPTD GSTGVELAPRSAEPGYLVTKVVAVDRDSGQNAWLSYRLLKASEPGLFSVG
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADSIPQVLADLGSLESFA
NSETSDLTLYLVVAVAVSCVFLAPFVILLALRLRRWHKSRLQLASGGGLTGAPASHFVGVD
GVQAF LQTY SHEVSLTTDSRKSHLIFPQP NYADMLVSQSEFEKSEPLLSGDSVFSKDSHGL
IEVSLYQIIFLFFFNCSV SQAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRD YRCKPPTVCLS
IYLSIYLSIYLSIYLLSCTDGS LTPVIPVLWEAEAGGSPEVGSLRPA

Signal sequence:

amino acids 1-30

Transmembrane domains:

amino acids 693-711, 809-823, 869-888

FIGURE 158

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAG
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA
TCAGTAGGTGACCCGCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCGACCTCGT
GCGGCCAAGACGTGGATGTTCTGCTCTTGCTGGGGGAGCCTGGGCAGGACACTCCAGGGC
ACAGGAGGACAAGGTGCTGGGGGTCATGAGTGCCAAACCCATTGCGAGCCTTGGCAGGCGG
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAGGTGGCAACTGGGTCCCTT
ACAGCTGCCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA
TAAAGATGGCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCTACAACA
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG
CACCGTCTCAGGCTGGGGCACTGTCACCACTCCCGAGAGAATTTCTGACACTCTCAACT
GTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA
GATGGCATGCTCTGTGCAGGCAGCAGCAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG
CCCCCTGGTGTGTGATGGTGCCTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC
ATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACCTCT
CTGGTTC

0075158.101501

FIGURE 159

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336
<subunit 1 of 1, 260 aa, 1 stop
<MW: 28048, pI: 7.87, NX(S/T): 1
MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVL
VGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSIHPPCYNSSDVEDHNHDLMLL
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPTLNC AEVKIFPQKKCED
AYPGQITDGMVCAGSSKGADTCQGDSGGPLVCDGALQGITSWGS DPCGRSDKPGVYTNI CRY
LDWIKKIIGSKG

Important Features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

007818-10101

FIGURE 160

GCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCGCCCCGGCCCCG
 CGCGCCGCCACGCCCCAACCCCGGCCCGCGCCCTAGCCCCCGCCCGGCCCGCGCCCCG
 GCCCGCGCCAGGTGAGCGCTCCGCCCGCGGAGGCCCGCCCGGCCCGCCCGCCCGCCCG
 CCCCAGCGCGCGGGGAACCGGGCGGATTCTCGCGCGTCAAACCACTGATCCCATAAAAC
 ATTCTATCTCCCGCGCGCCGCGCTGCGAGCGCCCCGCCAGTCCCGCGCCCGCGCCCGCTCG
 CCCTGTGCGCCCTGCGCGCCCTGCGCACCCGCGGCCGAGCCAGAGCCGCGGCGGAGC
 GGAGCGCGCCGAGCCTCGTCCCGCGGCCGGGCGGGGCCGCGTAGCGCGCGCGCTTGA
 TCGGACCCCGCGCGGGGAGACGGGCGCCGCCCGAAACGACTTTCAGTCCCGGACGCGC
 CCGGCCAACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTG
 CTGTGGCTGCAGGCTTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGA
 GCCAAGGTGACGACAAGCTGCCCGCAGCAGGCGCTGCAGGCTGTGCCCGTGGGCATCCCTG
 CTGCCAGCCAGCGCATCTTCTGCACGGAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC
 CGTGCTGCCGCAACCTCACCATCTGTGGCTGCACTCGAATGTGCTGGCCCCGAATTGATGC
 GGCTGCCTTCACTGGGCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC
 GGTCTGTGGACCTTGCACATTCACGGCCTGGGCGCCCTACACACGCTGCACCTGGACCGC
 TGGCGCTGCAGGAGCTGGGCCCCGGGGCTGTTCCGCGCCCTGGCTGCCCTGCAGTACCTCTA
 CCTGCAGGACAACGCGCTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCA
 CACACCTTCTTCTGCAGGCAACCGCATCTCCAGCGTGGCCGAGCGCGCCTTCCGTGGGCTG
 CACAGCTCGACCGTCTCCTACTGCACCAGAACCGGTGGCCCATGTGCACCCGCATGCCTT
 CCGTGACCTTGGCCGCTCATGACACTCTATCTGTTTGCCAAATCTATCAGCGCTGCCCA
 CTGAGGCTGGCCCCCTGCGTGCCTGCGTACCTGAGGCTCAACGACAACCCCTGGGTG
 TGTGACTGCCGGGCACGCCACTCTGGGCTGGCTGCAGAGTTCCGCGGCTCCTCCTCCGA
 GGTGCCCTGCAGCCTCCCGCAACGCTGGCTGGCCGCTGACCTCAAACGCTAGCTGCCAATG
 ACCTGCAGGCTGCGCTGTGGCCACCGGCCCTTACATCCCATCTGACCGGCGAGGGCCACC
 GATGAGGAGCCGCTGGGGCTTCCAAAGTGTGCCAGCCAGATGCCGCTGACAAGGCCCTCAGT
 ACTGGAGCCTGGAAGACAGCTTCCGCGAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTG
 ACAGCCCGCGGGCAACGGCTCTGGCCACGGCACATCAATGACTCACCTTTGGGACTCTG
 CCTGGCTCTGCTGAGCCCCGCTCACTGCAGTGCGGCCGAGGGCTCCGAGCCACCAGGGTT
 CCCCACCTCGGGCCTCGCGGAGGCGAGGCTTTCACGCAAGAACCGCACCCGACGCCACT
 GCCGTCTGGGCCAGGCAGGCGAGCGGGGTGGCGGGACTGGTGACTCAGAAGGCTCAGGTGCC
 CTACCCAGGCTCACCTGCAGCCTCACCCCTGGGCTGGCGCTGGTGTGTGGACAGTGCT
 TGGGCCCTCTGAACCCAGCGGACACAAGAGCGTGCTCAGCAGCAGGTGTGTGTACATAC
 GGGGTCTCTCTCACGCGGCCAAGCCAGCCGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAG
 GTCCTCCCTGATGGACGCTGCCGCCGCCACCCCATCTCCACCCCATCATGTTTTACAGGG
 TTCGGCGGACGCGTTTGTTCAGAACGCGCCTCCACCCAGATCGCGGTATATAGAGATAT
 GCATTTTATTTTACTTGTGTAATAATATCGGACGAGTGAATAAAGAGCTTTTTCTTAA
 AAAA

09076103 101501

FIGURE 161

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184
><subunit 1 of 1, 473 aa, 1 stop
><MW: 50708, pI: 9.28, NX(S/T): 6
MKRASAGGSRLLAWLWLQAWQVAAPCPGACVCYNEPKVTTSCTPQGLQAVPVGIPAAASQRI
FLHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPA
TFHGLGRLLTLLHLDRCGLQELGPGGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH
GNRISSVPERAFRGLHSLDRLLHQNVAHVHPHAFRDLGRMLTYLYLFANNLSALPTEALAP
LRLQYLRRLNDNPWVCDRCARPLWAWLQKFRGSSSEVPCLPQRLAGRDLKRLAANDLQGCA
VATGPHYPIWTGRATDEEPLGLPKCCQPDAAADKASVLEPGRPASAGNALKGRVPPGDSPPGN
GSGPRRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA
GSGGGGTGDESGSGALPSLTCSLTPLGLALVLWTVLGPC

Important features:

Signal peptide:

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

WFV domain

amino acids 411-425

FIGURE 162

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCTCTGGAGAGGACTAC
TCACTGGGCATATTTCTGAGGTATCTGTAGAAATAACCAAGCCCTCAGATACTGGGGACTTTAC
AGTCCACAGAACCGTCTCTCCAGGAAGCTGAAATCCAGCAAGAAACAATGGAGGCCAGCGGGA
AGCTCATTTTCAGACAAAGGCAAGTCTCTTTTCTCTCTCTTTTGGGCTTATCTCTGGCG
GGCGCGCGGGAACCTAGAAGCTATTCTGTGGTGGAGGAACTGAGGGCAGCTCCTTTGTAC
CAATTTAGCAAAAGGACTGGGTCTGGAGCAGAGGGAATTTCTCCAGCGGGGGGTTAGGGTTG
TTTCCAGAGGGAAACAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTTGTGTCTAAAT
GAGAAATTGGACCGTGAGGATCTGTGCGGTACACAGAGCCCTGTGTGTACCTTTTCCAAGT
GTTGTCTAGAGAGTCCCTTCGAGTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC
ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCTCTCTGGG
ACTACGTTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCGAAACAAATATTGAGAACTA
TATAATCAGCCCCAACTCTATTTTCGGGTCTCTACCCGCAACCGCAGTGATGGCAGGAAAT
ACCCAGAGCTGGTGCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAACA
CTCACAGCACTGGATGGTGGCTCTCCGCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT
CCTGGATGTCAACGATAATGCCCTGAAATTTGAGCAGCCCTTTCTATAGAGTGCAGATCTCTCC
AGGACAGTCCGGTAGGCTTCTGGTTGTGAAGGTCTCTGCGCAGGATGTAGACACAGGAGTC
AACGGAGAGATTTCTTATTCATTTTTCAAGCTTCAGAAGAGATTGGCAAAACCTTTAAGAT
CAATCCCTTGACAGGAGAAATGAACTAAAAAACAACCTCGATTTTCGAAAACTTCAGCTCT
ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACTTTTTCTGGAATAATGCACCGTTCTGATTT
CAAGTGATAGATGTGAACAGCACCATGCCCCAGAAGTTACCATGTCTGCATTTACAGCCCAAT
ACCTGAGAAACGCGCTGAAACTGTGGTTGCATTTTTCAGTGTTTCAGATCTTGATTGAGGAG
AAAATGGGAAAATTAGTTGCTCCATTGAGGAGGATCACCTTCTCCTGAAATCCGCGGAA
AACTTTTACACCTACTAACGAGAGAGACCACTAGACAGAGAAAGCAGAGCGGAATACAAAT
CACTATCACTGTCACTGACTTGGGGACCCCTATGCTGATAACACAGTCAATATGACCGTGC
TGATCGCCGATGTCAATGACAACGCTCCCGCCCTTCACCAAACCTCTACACCCTGTTCTGTC
CGCGAGAACAAACAGCCCCGCCCTGCACATCCGCAGCGTCAGCGCTACAGACAGAGACTCAGG
CACCACCGCCAGGTACCTACTCGCTGCTGCCGCCAGGACCCGCAACCTGCCCTCACAT
CCCTGGTCTCCATCAACGCGGACAAACCGCCACCTGTTGCGCCTCAGGTCTCTGGACTACGAG
GCCCTGCAGGGTTCCAGTTTCCGCTGCCGTGGGCGCTTCAGACCAACGCTCCCCGGCGCTGAGCAG
CGAGGCGCTGGTGCGCGTGGTGGTCTGGACGCCAACGACAACTCGCCCTTCTGTGCTGTACCC
CGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCGGGCGGCGGAGCCGGGCTAC
CTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCTGGCTGTCTGTACCA
GCTGTCTCAAGGCCACGGAGCTCGGTCTGTTCCGGCTGTGGGCGCAACAATGGCGAGGTGCGCA
CCGCCAGGCTCTGAGCGAGCGCAGCGGCCCAAGCACAGGCTGGTGGTGTGGTCAAGGAC
AATGCGAGCCCTCCGCTCGGCCACCGCCACGCTGCAGTGTCTCTGGTGGACGGCTCTCTC
CCAGCCCTACCTGCTCTCCCGGAGGCGGCCCCGACCCAGGCGCCAGGCGCATTTGCTCAGCG
TCTACCTGGTGGTGGCTGGCCCTCGGTGTCTTCGCTCTTCTCTTTTCTGGTGTCTCTGTTT
GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCCCTCGGTGGGTGCTGTGTTGGTGCCTG
GGGCCCCCTTCCAGGGCATCTTGTGGACATGAGCGGACCAAGGACCTATCCAGAGCTACC
AGTATGAGGTGTGTCTGCGAGAGGCTCAGGACCAATGAGTTCAAGTTCCTGAGACGGCTATT
ATCCCCAATCTCCCTCCCACTGCTGGGAAAGAAATACAAGGAAATTTCTACCTTCCCCAA
TAACTTTGGGTTCAATATTCACTGACCATAGTTGACTTTTACATTCCATAGGTATTTTATT
TGTGGCATTTCCATGCCAATGTTTATTTCCCCCAATTTGTGTGATGTAATATGTACGGAT
TTACTCTTGATTTTTCTCATGTTCTTTCTCCCTTTGTTTTAAAGTGAACATTTACCTTTATT
CCTGGTTCTT

09978760 105101 8818760

FIGURE 163

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314
<subunit 1 of 1, 798 aa, 1 stop
<MW: 87552, pI: 4.84, NX(S/T): 5
MEASGKLICRQRQVLFSLFLGLSLAGAAEPRSYSVVEETEGSSSFVTNLAKDLGLEQREFSR
RGVRVVSARGNKLHLQLNQETADLLNEKLDREDLCGHTEPCVLRQVLLSEPFEEFFQAEQV
IDINDHSPVFLDKQMLVKVSESSPPGTTTFLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNAPEFEQPFY
RVQISEDSPVGFLVVKVSATDVDTGVNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF
EKLQSYEVNIEARDAGTFPSGKCTVLIQVIDVNDHAEVMTSAFTSPIENAPETVVALFSVS
DLDSGENGKISCISIQEDLPFLKSAENFYTLTTERPLDRESRAEYNITITVTDLGTPMLITQ
LNMTVLIADVNDNAPFTQTSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLLPQDP
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELGFLGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLEAAPTQAA
ADLLTVYLVVALASVSSLFLFSVLLFVAVRLCRRSRASVGRCLVPEGPLPGLHVDMSGTRT
LSQSYQYEVCLAGSGTNEFKFLKPIIPNFPQCPGKEIQGNSTFPNNFGFNIQ

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 685-712

Cadherins extracellular repeated domain signature.

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

ATP/GTP-binding site motif A (P-loop).

amino acids 285-292

N-glycosylation site.

amino acids 418-421, 436-439, 567-570 and 786-789

FIGURE 164

ACCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCGCTAGCCGTGC
GCGGATTGCCTCTCGGCCCTGGGCAATGGTCCCGGCTGCCGCTGACGACCGCCCCGCGTCAT
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCCTCCGCGGCGTGG
AGGTTGCAGAGGAAAGTGGTTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG
TGATTCTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT
GGAGGAGCGGAGGACTCAAGGTGCAACGTCGAGAGAGCCTTTTCTCTGGATGGCGCTGG
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG
GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTCACAGGACCT
TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCTCTGTTTACACCCCGTGGT
GCCGCTTTTCTGCCAGTTTGGCCCCCTCACTTTAACTCTCTGCCCGGGCATTTCAGCTCTT
CACTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC
TGTTCTCAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATACAGATC
GAACTGGAACACTGAAAATCTTCATTTTAAATCAGACAGGTATAGAAGCCAAGAAGAAT
GTGGTGGTAACTCAAGCCGACCAATAGGCCCTCTCCAGCACTTTGATAAAAAGTGTGGA
CTGGTTGCTGTATTTTCTTATTCTTTTAAATAGTTTTATTATGTATGCTACCATTGAA
CTGAGAGTATTGCGTGGCTAATTCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT
GAAAGAAGTTGAAAAGAGGAACTTCAATCCTTCGTTTCAAGAAATTAGTGCTACAGTTTCATA
CATTTTCTCCAGTGACGTGTTGACTTGAAACTTCAGGCAGATTAAAGAATCATTTGTTGAA
CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC
AAAAATATTCAATAG

00075128.101501

FIGURE 165

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333
><subunit 1 of 1, 360 aa, 1 stop
><MW: 39885, pI: 4.79, NX(S/T): 7
MVPAAGRPRPRVMRLLLGWVQLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEE
ELLHDPMGQDRAAEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTGAGGAEDSRC
NVRESLSLDGAGAHFPDREEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE
NFTLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPPALHFLALDAS
QHSSLSTRFGTVAVPNILLFQGAKPMARFNHTDRLTLETLKIFIPNQTGIEAKKNVVVTQADQ
IGPLPSTLIKSVDWLLVFSLSLFFLISFIMYATIRTESIRWLIPGQEQEHVE

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 321-340

Homologous region to dilsufide isomerase

amino acids 212-302

N-glycosylation site.

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281
and 293-296

Thioredoxin domain

amino acids 211-227

FIGURE 166

CCC GGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCACGATGCTGCAGGGCCCTGGCT
CGCTGCTGCTGCTCTTCTCGCCTCGCACTGCTGCCCTGGGCTCGGCGCGGGGCTCTTCTC
TTTGGCCAGCCCGACTTCTCTACAAGCGCAGCAATTGCAAGCCCATCCGGTCAACCTGCA
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCA^ΔCCTGCTGGGCCACGAGACCA
TGAAGGAGGTGCTGGAGCAGGCCGCGCTTGGATCCCGCTGGTTCATGAAGCAGTGCCACCCG
GACACCAAGAAGTTCTGTGCTCGCTCTTCGCCCCCGTCTGCCTCGATGACCTAGACGAGAC
CATCCAGCCATGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGCCCCGGTTCATGTCCG
CCTTCGGCTTCCCCTGGCCCCGACATGCTTGAGTGCACCGTTTCCCCCAGGACAACGACCTT
TGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG
ATTTTGCACTGAAAAATAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAAATCATC
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCGGAAGGGACCTGAAGAA
ATCGTGCTGTGGCTCAAAGACAGCTTGCAGTGCACTGTGAGGAGATGAACGACATCAACG
CGCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTA
GTCCCGGCATCTGATGGCTCCGACAGGCTGCTCCAGAGCACGGCTGACCATTTCTGCTCC
GGGATCTCAGCTCCCGTCCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT
TCCCCCTGCCTTTTGACGTTTGCACTCCCAGCATTTCTGAGTTATAAGGCCACAGGAGTG
GATAGCTGTTTTCACCTAAAGGAAAAGCCACCCGAATCTGTAGAAATATTCAAACATAATA
AAATCATGAATATTTTAA

0973160 "161501

FIGURE 167

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920
><subunit 1 of 1, 295 aa, 1 stop
><MW: 33518, pI: 7.74, NX(S/T): 0
MLQGPGSLLLFLASHCCLGSARGLFLFGQPDFSYKRSNCKPIPVNLQLCHGIEYQNMRLPN
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDDETIQPCHS LCVQVKDR
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDNDNDIM
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLNQVSRDLKKSVLWLKDSLQCTCE
EMNDINAPYLVMGQKQGGELVITSVKRWQKGQREFKISRISIRKLQ

Important features:

Signal peptide:

amino acids 1-20

Cysteine rich domain, homologous to frizzled N terminus

amino acids 6-153

09070188.101501

FIGURE 168

GTGGAGGCCGCCGACGATGCGGGGCCGACGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG
CCCTGTGCGCGCAGCGGGGCCACCGACCTACGCGCGCCGCTGGGTGTTCTGTCTCGCGATC
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT
TGCTGAGGACTTGGTCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTCGGGCTCCGTGCGGCG
ACCATCTCGGGTGCCTGGCTGAACTTTGCCGGGAGTGTGTACGCATGGTGCCTGCATGGT
TGTGGGACCCAAACCCATTGCTCTTCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCACAGAGCACACAGCGA
GCCACGGCCAACATGCTCGCCACCATGTGCAACCCCTCTGGGCGTCTTGTGGCCAAATGTGCT
GTCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCGGTTAATGCTCGGTGTCTATACCATCC
CTGCTGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCACCCTCG
CCCTCTGCCGGGGTGGCAGCTCCACCTCAGAGAAGTTCTGGATGGGCTCAAGCTGCAGCT
CATGTGGAACAAGGCCTATGTCATCTGGCTGTGTGCTTGGGGGAATGATCGGGATCTCTG
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTC
GGCCTCTGTGGCGCTCTCTTCATCAGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCTTA
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTTCTCTCTGG
CCTGCGTGCCCTTTGGCCCTGGTGTCCAGCTGCAGGGACAGACCCTTGGCCCTGGCTGCCACC
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTGGA
GTGTTCCCTTCCCCGTGGGGGAGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG
AGGGAATACTCATCATGTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGCTCCTTG
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCGG
CCTGTGCACCTTCTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGGCGCCTGC
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCTTGGGGCCAGCAGCGGCACTCCGGA
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCGGAGCCCCCACCAGCCT
GCCACCGAGCGACTCCCCGTGCGCAAGGCCACGACGCCAGCGCCCTCCCGCCCGCGC
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGCTGGGTCTCACTCCTCCTT
CTCCTCCCCGTGGGTGATCAGCTAGCTGAGCGCCTTGTAGTCCAGGTTGCCCGCCACATCGA
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGCGAAAGGGCTCCTTGCGGGCT
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

097518.10501

FIGURE 169

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988

><subunit 1 of 1, 560 aa, 1 stop

><MW: 58427, pI: 6.86, NX(S/T): 2

MAGPTEAETGLAEPRALCAQRGHRTYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV
LSMEQINWLSLVYLWVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTQN
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPPEHQRATANMLATMSNPLGVLVANVLSPLV
KKGEDIPLMLGVYITPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA
YVILAVCLGGMIGISASFSALEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK
HFTEATKIGLCLFSLACVPFALVSQLQGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV
GEGAATGMIFVLGQAEGLIMLMTALTVRSEPSLSTCQQGEDPLDWTVSLLLMAGLCTFF
SCILAVFFHTPYRRLQAESGEPSTRNAVGADSGPGVDRGGAGRAGVLGPSTATPECTARG
ASLEDPRGPGSPHPACHRATPRAQGPAAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSFPWVIT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,
280-300, 318-337, 341-357, 375-387, 420-441

N-glycosylation site.

amino acids 40-43 and 43-46

Glycosaminoglycan attachment site.

amino acids 468-471

FIGURE 170

GTCCACATCCTGCTCAACTGGGTCAAGTCCCTCTTAGACAGAGCTCTTGTCCATCATTTTGTCTGAAGTGGACCAAC
 TAGTTCCCGCAGTAGGGGTCTCCCTCTGGCAATTTCTGTATCGGGCTTTGGACATCTCAGATCGCTTCCAACTGAAGA
 TGGCTTGGCTTGGGGGCTCTGTCTGTCTTTCATAATCATCTAACTATGGGACAGAGGTGTGTCGCGGCAGCTCTGCGGG
 AAGGAGCAGCGGGCTGTATCAAGCCATCCAGGAAACATCGGAGGACTTCTCAGCTTGAAGAACTCTAGTGGTT
 CTCTGAATCTAGCCCATTTGGCGGTAAAGCATATGCAACTCTTCTGCAACTCTCTGCTGGGGCTTTTGGGGCGAGTGG
 TCTATTATTCTTTTAGGGAGTTGTCAAGAGGTGACCATCTCTCAGCGTGAATTAACCAAGTGTCTAGAGGAGTGGCC
 ATCTGTGTACAGTGTATCGGGAAGCTCTCCAGGAAGCTGGGCGGGAGGAGGCGGAGGCAAGCTGCGGGCGCGCTT
 CAGAGTCTTGCGAGCTGCTCAGGCGCTCCCATTCAGGTGAGCTCTGAGGAGAGGCTTGTCTGACACAGGCGAGGG
 GCTGGATCGAGAGAGCTGTGCGGACAGTGGGACTCCGTCTGGTTTCTTTGATGTGCTTGACACAGGGGATTT
 GGTCTGTATGCTCATGTGGAGATCCAAGTGTCTGGACATCAATGACCAACAGGCAAGGTTTCCCAAAGGCGAGACAGGA
 GCTGGAAATCTCTGAGAGCGCTCTCTGCGAAACCCGGAATCCCTCTGGACAGAGCTCTTGACCCAGACAGAGGCC
 TAAACCCCTGACACCTCACTCTGTCTCCAGTGAGCACTTTGCCCTTGGATGTCTATGTGGGCGCTGATGAGAC
 CAAACATGCGAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAATCCATTCAATTTTTGATCTGGTGTAACTGC
 CTATGACAATGGGAACCCCCCAAGTCAAGGTACAGCTTTGGTCAAGGTCAACGCTTTGGATCCAATGACAAATAG
 GACGCCACAGACCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCTCAGTAAAGCATGCTCCAGCAAGCT
 GCTGGACACCTTCAGTATTGATGCAAGACAGGCGAGGTCAATCTGCTGCTGACCTCTAGACTATGAAAGAAACCC
 TGCTCTCAGAGTGGATTTCTCAGGCAAGGGGACTCTGGGTCCAATCCTATCCAGCCATTTGCAAAAGTTCTCTACAA
 GGTCTTGGATGTCAATGACAACTCCCAAGCATCCAGCTCACTGGGCTCCAGGACATCTGGTGTGAGAAGC
 TCTTCCCAAGGACAGTTTATTGTCTTGTCTATGCGAGTACTTGGATCTCAGGACACAAATGGTTTGGTCTCACT
 CTGGCTGCTCAAGAGCTGGGCACTTCAGGCTGAAAAGAACTAATGGCAACACATACATGTGTCTCAACAAATGC
 CACATGGAAGAGAGGAGTGGGCCCAATATACCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATC
 AGCCAGAGAAACAGCTCAGCATTCAGATCAGTGAACATCAAGCAAACTGACCTGTGTGGAAGAAAGCAGGTATGA
 AGTCTCCAGCGGGGAAACAACTTACCCTCTTCCACTTATACCATCAAGGCTCATGATGCAAGCTTGGGCAT
 TAATGGAAAGTCTCATACCGCATCCAGGACTCCCGATTTGCTCATAGTAGTCTTACGATCCAAACAGAGGA
 GGTCACTGTCTAGAGGTCTCACTGAATCATGAAGAGATGGCGGGTTTGTAGTTCCAGGTGATCGCAGAGGACACGG
 GCAACCCCTGTGATCTGATCTGATCTCTGTGTGGGCTCAGCTCTTGGATGCAAGTATGATATGAAAGTGGTGT
 CCAGCCTGTGCTCAGCGATGGAAAGCCAGCCTCTCCGTCTCTGTGAATGCTCTCAAGGCCACCTGCTGGTGGCC
 CTCTGAGACTCCCAATGGCTTGGGCGGAGGGGCACTGACACACTCTCACTGGGCACTCAGAGCTCCCGGCCAT
 CCTTTTGAACCAACTTGTGCGAAGAGATGAGACTCGGGGCAATGAGAGGCGCTCTACAGCATCCGCAATGG
 AAATGAAGAGCACTCTCTTCACTCTCAACCTCTCACTCGGGGCACTGTCTGATGCTCAACATGTCCAGCAGCCT
 GATGTGGAGTGTGATGGGAGCTGGAGATAGTAGTAGAGGACAGGGGAGGCCCGCTTACAGACCCGAGGCGCTGT
 CAGGTCATGTGTTTGTCAACAGTGTGAGCAACCTGAGGCACTCAGCGCGCAAGCCTTGGGCTTGGAGCATGTGAT
 GCTGACGCTGTCTGCTGCTGTGATCTTGTGGGCACTCTTGGGTTGATCTTGGTCTCATGTCCATCTGCGCG
 GACAGAAAGAGAGACAAAGAGGCTCAACCTGTCTGGGAGGCGGAGTCCACTTACCGCCAGCAGGCCAAGAGGCC
 CCAGAAACACATCTCAGAGGACAGACATCCACTCTGTGCTCTGTGCTCAGGGGTCCAGGCGGCTGTGTGAAT
 CGGCGAGTCCCAACAGATGTGGACAGGAGGCGATGATGGAAGCAGGCTGGGACCCCTGCTGAGGCGCCCTT
 CCACCTCAACCCGACCTGTGACAGGCTGTGCTAATCAAGGCAACAGGGGACACCGGCGAGAGCCGAGAGGT
 GCTGCAAGACACCTGTCAACCTCTTTCAACCATCCAGGACAGAGGAATGCTTCCCGGAGGACCTGAACTCTTC
 CGAGCCCGAGCTCTGACAGGCGGAGGCACTGCTCCAGGCTCTGAAGGTTGACGAGGCGCCCAAGGAGGCTGCG
 TGGAGCTCAGGCGAGTGAAGAGCCCCACAGAGGCCACAGGCTCTCTCTGCAACCTGAGACGCGAGCATCT
 CAATGCAAAATGTCTCCCTGAGAAAGAACTCAGGCGCCCTGAGTCTCTGGGCTTGTCTCATGTCTGTCGTGCG
 GTCTTCTGCGCGAGCGGAAACCCGTGGAGGAGCTCACTGTGGATTTCTCTCTGTCTCAGCAATCTCCACAGTGTCT
 TGTCTTGTCTGATCCTGAGGCAATCCAGGCCAATCCAAACCAAGGAGAAATAGTACTTGGCCAAAGCCAGGAGG
 CAGCAGGAGTGCATCCAGACACAGATGGCCCAAGTGAAGGGCTGGAGGCGCAGACAGACAGAAACAGGAGGA
 AGGGCTTTGTGATCTTGAGAGGAGCTCTCTGTGAAGCACTGCTAGAAGAGAGCTGTCAAGTCTGTCTGGAACC
 CAGCAAGTGTCTGCGCTGGACCGGCTGAGCGCCCTGACCGGCGCTGGATGGCGAGACTCTTTTGCCCTTCA
 CCAACTACCGTGACAAATGTCTCTCCCGGATGCTGACGACACAGGAGGAGGAGGAGCTTCCAGAGCTTGGC
 CAGGCGAGGCGACAGAGCTGAGCGCCCAACAGGACAGGAGCTGGCGAGCACTTTGTCTCGAGAGTGAATCTACT
 GCTGAGAGTGTCTGCTGGAACAGGCTCCAGCATGCGCGTGGAGGCGCTCCGAGGCGCTCTGCGGCGCTCTCTG
 CTGCGGGAGGACCTCAGTTTATGACTTGGCCACCACTGCTCAGGCTCAGGCTGAAGTGAAGGAGGAGCCAGGCT
 AAGAAGCGGAGTCTGAGGCGAAGGACAGGCGAGCAGCAGTGTGCTGTGACATATCTCAGAGCGCT
 CTGATCTCAAGAAACAGGGGCTCAGGATCTGTGACAGAGCTGGTTTCAAAATCTTGTAACTCACTAGCTAG
 CGCGGCTGTGAACTTATGGGTGACTGATGCTACCCCAAGAGGAGGCGGAGGCGGAGGCTCAACAGCTGAC
 TGACCAAGAGCGCCCTTGTGAAGCAGCTGTGATCTTTTGGAGGACAGGAGCGGTTTGTGCTGAGATAGATGTT
 TCTCTGCAAAACATATGTGGAGCAAAAGGCTCAGTCTCTGCGAAGACAGATGCGCAGGATATCAGGACAG
 AAGGCTGGCTTCTTGGGTAGCAGGAGTCAAGGGGCTGTACCTTGGGGTGGCAGGAAATGCTCTGACCTAT
 CATAAAGGAAAGCAGTAAAAAAGAAAAAAAAA

10510155.101501
 36978155.101501

FIGURE 171

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331
<subunit 1 of 1, 1184 aa, 1 stop
<MW: 129022, pI: 5.20, NX(S/T): 5
MMQLQLLLGLLPGGYLFLLGDCQEVTTTLTKYQVSEEVPSGTVIGKLSQELGREERRRQA
GAAPQVLQLPQALPIQVDSEGLLSTGRRLDREQLCRQWDPCLVSFVVLATGDLALIHVEIQ
VLDINDHQPRFPKGEQELEISESASLRTRIPLDRLDPDTGPNLTHTYTLSPSEHFALDIVI
GPDETKHAELIVVKELDREIHSFFDLVLTAIDNGNPPKSGTSLVKVNVLDSDNSPFAFAESS
LALEIQEDAAPGTLIIKLATDPDQGPNGEVEFFLSKHPPEVLDTFSIDAKTGQVILRRPL
DYEKNPAYEVDVQARDLGNPIPAHCKVLIKVLDVNDNIPSIHVTWASQPSLVSEALPKDSF
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLAQD
QGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHADLGGINGKVS
YRIQDSPVAHLVAIDSNTEGVTQAQRSLNIEEMAGFEFQVIAEDSGQPM LASSVSVMVSL LDA
NDNAPEVVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPLATHSSRPFLLT
I VARDADSGANGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK
KDNRAYNCREAESTYRQPKRPQKHQKADIHLVPVLRGQAGEPCEVGGQSHKDVKKEAMMEA
GWDPCQLQAPFHLTPTLTYRTLNRNQGNQGAPAESREVLQDTVNLLFNHPRQRNASRENINLPEP
QPATGQPRSRPLKVAGSPTGRLAGDQGSEEAPQRP PASSATLRRQRHLNGKVSPEKESGPRQ
ILRSLVRLSVAFAERNPVEELTVDSPPVQQISQLLSLLHQGQFPKPNHRGNKYLA KPGGS
RSAIPD TDG PSARAGGQTDPEQE EGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPD
PAWMARLSLPLTNTYRDNVISPDAAATEEPRTFTQFGKAEAPELSPTGTRLASTFVSEMSLS
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSDLATSAASGMKVQGDGPGKGTGTEGKSRGSS
SSSRCL

Important features:

Signal peptide:

amino acids 1-13

Transmembrane domain:

amino acids 719-739

N-glycosylation site.

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

Cadherins extracellular repeated domain signature.

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCAGTCCCGGCTGCAGCACCTGGGAGAAGG
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGAGTGGGAAGTGGAG
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT
CCCAGATACTATTTTTTGGATTGGGTGGCTTTCTTCATGCGCCAATTGTTTAAAGACTAT
GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGCAACCAT
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT
GGAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTTCATGGTGCTTTTTTACATTGGC
TATTTTATTGTGAGCAATATCCGACTACTGCATAAAACAACGACTGCTTTTTTCTGCTCTCTT
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGTTGGTGTGATTGGAGTGACTCTC
ATGGCTCTTCTTCTGGATTTGGTGTGTCAACTGCCCATACACTTACATGTCTTACTTCTCT
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAAACCATGGATA
TGATCATAAGCAAAAAGAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAA
GTGCATAACAACCATCAGGTTTCTGGGAATGATAAAAAGTGTTACCCTTCAGCATCAGG
AAGTGAATATCTTACTCTTATTCAACAGGAAGTGGATGCTTGGAGAATTAAGCAGGCAGC
TTTTTCTGGAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC
AAGGGGAATATTTTAATTTTCTGGTTACTTTTTCTCTATTACTGTGTTTGGAAAAATTT
CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCAAGAGGCA
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATT
TCCTTCATTCTTGTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCAATTGTCTCTGCTATTAGCAC
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCCTTTAGAA
TACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTT
TGATGTGATCTTCTGGTTCAGCGCTCTCTAGCATACTCTTCTCTATTTTGGCTCACAAAC
AGGCACCAGAGAAGCAATATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGT
GGTTTCAAAATTTAGATATAAGAGGGGGGAAAAATGGAACAGGSCCTGACATTTTATAAAC
AAACAAAATGCTATGTTAGCATTTTTCACCTTCATAGCATACTCTTCCCGTCAGGTGATA
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAACTACTCA
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAGAAACTAA
AGGTGAAAAATACACTGGAACCTCTGGGCAAGACATGTCTATGGTAGCTGAGCCAAACAGCT
AGGATTTCCGTTTTAAGGTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT
AAAATCAGAGACTGTAACAAAAAAAAAAAAAAAAAAAGGGCGGCCGACTCTAGAGTCG
ACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

FIGURE 173

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI
LGVLNSSSRYPFHWMNLCVILLILVFMVPPYIGYFIVSNIRLLHKQRLLFSCLLWLTfMYFF
WKLGDPPILSPKHGILSIEQLISRVGVIGVTLMAALLSGFGAVNCPYTYMSYFLRNVTDTDI
LALERLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ
QEVDALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF
DRVGKTDPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTkFFYAISs
SKSSNVIVLLLAQIMGYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA
LSSILFLYLAHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

ENCLOSURE

GTGTGCGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCTTAAAAATTTGGCCAAGGGTTTC
TTTNTTGAATTCGGGTTNNGNATACCTTCCCAGAAAATATTTTTTGGATTGGGGTAGNTT
TTTTTCATGCGCCAAATGTTTAAAGACTATGAGATACGTGATATGTTGTACAGGTGATNTT
NTCCGTGACGTTTGCAATTTCTTGCACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAATAAGCACTGTGTGTAATCTGCTGATC
CTGGTTTTCATGGTGCCTTTTTACATTTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA
TAAACAACGACGTCTTTTCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAN
TAGGAGATCCCTTTCCCACTTC

THE UNIVERSITY OF CHICAGO

FIGURE 177

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL
QPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMQKESKENQWL
GVSVRSQGGPKIVTCAHRYEARQQRVDQILETRDMIGRCFVLSQDLAIRDELDDGGGEWKFCBG
RPQGHQPGFGCQQGTAAAFSPDSHYLLFGAPGTYNWKGATARVELCAQGSADLAHLDDGGPYEA
GGEKEQDPRLLIPVPANSYFGFSIDSGKGLVRAEELSFVAGAPRANHKGAVVILRKDSASRLV
PEVMLSGERLTSFGFGYSLAVADLNSDGNPDLLVGAFFERQBELGGAVVYVNLQGGHWAGI
SPLRLCGSPDSMFGISLAVLGDNLQDGFPDIAVGAPFDGDGKVFITYHGSSLVGVAKPSQVLE
GEAVGIKSGFYSLSGSLDMDGNQYPDLLVGS LADTAVLFRARPILHVSHEVSIAPRSIDLEQ
PNCAGGHSVCVDLRVCFSYIAVPSSYSPTVALDYVLADTDRLRGQVPRVTFLSRNLEEPK
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSSYSLQTPRLRRQAPGQGLPPVAP
ILNAHQPSPTQRAEIHFLKQCGGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA
LSGQPVI GLELMTNLPSPDPAQPQADGDDAHEAQLLVMLPDSLHYSVGRALDPAEKPLCLSN
ENASHVECELGNPMKRGAQVTFYLLISTSGISIEETEEVELLATISEQELHPVSARARVF
IELPLSIAGMALPQQLFFSGVVRGERAMQSERDVGSKVKYEVTVSNQGGQSLRTLGSFAFLNIM
WPHEIANGKWLPLYPMQVELEGGQGPQKGLCSRPNILHLDVDSDRRRRRLELEPEQPEPGE
RQEPSMSWWPVSAAEKKNTLDCARGTANCVVFSCLYPSFDRAAVLHVWGRLWNSTFLEEY
SAVKSLEVI VRANITVKSSIKNLMRLDASTVIPVMVYLDPMMAVVAEGVPPWVILLAVLAGLL
VLALLVLLLWKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKKEKTGTILRNNWGSPPREGP
DAHPIAADGHPHGLPGDGHGPGGTA

Important features:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

FIGURE 179

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829
><subunit 1 of 1, 436 aa, 1 stop
><MW: 49429, pI: 4.80, NX(S/T): 0
MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR
DEVEDDYFRTWSPGKPFDDQALDPAKDPCLMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCCPCP
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKTKTLRLPERSRFDTSILPI
CKDSLGMFNRDLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ
RQQDPPCQTELSNIQKRQGVKKLLGQYIPLCDEDEGYKPTQCHGSVGGCWCVDRYGNEVMGS
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDDEDEGDDDDGGDDHDVYI

Important features:

Signal peptide:

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

FIGURE 180

CAGACTCCAGATTTCCTGTCAACCCAGGAGGATCCAGAGAGGAAACGCGGAGCGGAGACAAACAGTACCTGACGC
 CTCTTTCAGCCCCGGGATCGCCCCAGCAGGGATGGGGCGACAAGATCTGGCTGCCCTTCCCGTGCCTCTCTGCGCC
 GCTCTGCCTCCGGTGTGCTGCTGCTGGGGCGCGGGCTTCACACCTTCCCTCGATAGAGCTCTCACCTTTACCTCT
 CCOCGCCGCAAAAGTAGGCTCTTACCAGCCCATGCCCTGAAGSCTCGCTGAGCATCGATACCAAGTTTTTA
 GATGGAGCAGGATAGATATTTGATTTCCTCTTGCCCTTCCAGAAAGGCAAAACCTTAGTTTTTGAACAAAGAAAA
 TCGATGTGAGTTTCACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTTGACAAATACATTACAGCACCATT
 TCTGAGAAAGTGATTTCTTTGAATTAATCTGTGATAATATGGAGAACAGGCAACAGAACAGAGGATTTGAGAG
 AAATATATTACTGGCAAGATATATTTGGATATGAACTGGAGAGCATCTCTGGAATTCATCAACAGCATCAAGTCC
 AGACTAGGCAAAAGTGGGCAATCAAAATTTGCTTAGAGCATTTGAAGCTCGTGATCGAAACATACAGAAAGGC
 AACTTTGATAGAGTCAATTTCTGCTCTATGTTAAATTTAGTGGTCACTGGTGGTGGTGTGACGCATTCAAGTTTAT
 ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAGTAGAACTTAAAACTCCAAAACATAGAGTACGTAACATTGAAA
 AATGAGGCATAAAATGCAATAAATGTTACAGTCAAGACCAATTAAATGGTCTTTCTCCAAAATATTTTGAGATATA
 AAAGTAGGAAACAGGTATAATTTTAATGTGAAAATTAAGTCTTACITTTCTGTGCAAGTAACTCTGCTGATCCAG
 TTGTACTTAAGTGTGTAAACAGGAATATTTTGAGAATATAGGTTTAACTGAATGAAGCCATATTAATAACTGTCAT
 TTTCTTAACITTTGAAAAATTTTGCAAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCGCTAATTGCAACACC
 AGTCTGTTTTTAAACAGGTTCTATTACCCAGAACTTTTTTGATAATCGCGGAGTACAAAATTAACCTGGGAAGTT
 TCAGTTTTTAAGTTATAAATCACCTGAGAAATTAACCTAATGATGGATTGAATAATCTTTAGACTACAAAAGCCCAA
 CTCTTCTCATTTTACATATGCTATCTCTCTATAATGTAATAGATAATAGCTTTGAAATTAACAATTAGGTTTTTG
 AGATTTTTATAACCAAAATACATTTCACTGTAAACATATTAGCAAAAGCATTAGTCTTTGTACTTTTACTTTTAACT
 CCAAAGCTGACATTTTCAAGTCTTAAAAACACAAAGTTACACTTACTAAAATTAGGACATGTTTTCTCTTTG
 AAATGAAGAAATATAGTTTTAAAGCTTCCCTCTCATAGGGACACATTTTCTAAACCTTAACTAAAGTGTAGGA
 TTTTAAATTAAGTGTGAGGTAAATAAGTTTATTTTTAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA
 TAATCATGTTTATGTTAAATTTAACATGATGTCTGACTTGGATAATTCATTATTAACAGCAGTTATGAAGGAAATA
 TTGCTAAATGATCTGGGCCACCATAAATAAATATCTCTTCTGAGCTCTAAGAAATATACAGAAACAGGAA
 AGAATTTAGAAAACTTGAGAAAACTAATCCAAAATAAAATTCATTAAGTAGAATCTAAATAAATATCTAGA
 ATCTGACTGGCTCATCATGACATCTTACTCATAAACATAAATAAAGAGATGATTAATTTTCCAGTTAGCTGGAG
 AAATTTGGCTGTAGGTTTTTATTTTCTCAAGAATTTCTGGTTTGAATTTTGTGAAGCAGGTACATTTTTATA
 AAATGTAGGCCCTATCTGTAAGTTTTAGCACTGGGTGTACATATTTTATAAAATTTTATATAACAACTTTATA
 TAAAAATGACCTTTCTGAACACTTTATTTTATGATGTTGAAGTAAGGATTAGAAACATAGACTCCCAAGTTTTAA
 CACCTAATGTGAATAACCCATATAACACAAAGTTTCTGCCATCTAGCTTTTTGAAAGTCTATGGGGCTTAC
 TCAAGTACTAGTAATTTAACTTCTATCATGAATGAATATAATTTTTAAGTTATGCCATTTATAACGTTGTTAT
 GACTACATTTGAGTTTGAAGAACAACTTAAATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAAAT
 CTGATAGCAATAATGATAACAGAGAGTGATTTCAATTACATCTCATAGTAGTATAAAAAGAGATACATTTCCC
 TCTTAGGCCCTCGGAGAGAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAAAATGAGGTAAATGGCGGT
 ATGATCAATTAACCTTAATGGCCAGAGAAATGCTTCAGGTGTCTAGGGGTATCCCTTGCAACACTTGCAAGACAA
 AGGTCAATAAGATCTTGGCTATGAATACCCCTCCCTTTTGGCTGTGTAATTTGCAATGAGAAGCAAAATTTACA
 GTACCATCACTAATAAAGCAGGCTACAGATATAAATCTGTCATCTTTCTATAAACTGTGATTAAGAATTTCTA
 CCTCTCTGATGGCTGTACTGTACTGTACTCTCTGACTCTTACCTAACATGAATTTGTTACATATCTCTCT
 ACATGTATGATTTGTGCCACTGATCTTAAACCTATGATTCAGTAACTTTTACCATATAAAAACGATAATTTGCTT
 TATTTGGAAGAAAGATTTAGGAATACTAAGGCAATTAATTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG
 CATAACCAAAAAAGCAAACTTTGAACAGAGTAAAACTTTAATATTTTAAAGACATACTGTTTATCTGCTT
 CATATGCTTTTTTAAATTTTCACTATCTCAATTTCTAAATTAAGTTTATGCTAAATGAGTAACTGTTTATCACTT
 AACAGCTCATTTTGTCTTTTCAATATACAAAATTTAAATACTACAATAATTAACCTAAGGCCCAACCGGATTC
 CATATGTTGACAGTTACCGGTTCACCTCAACCTAAGGCCCTAGAGTTTGTCTGATGATCTTGATGATTAAT
 GTTATGCTGTCTTCTCATGTGAATGTCAAGACATGGAGGGTGTGTTAAATTTTATGTTAAAAATTAATCCCTCTTA
 CACATAAATGGTGTCTTAAAAATTTGACAAAAATGAGCACTTACAATGTATGTCTCTCCCTCAAAATGAAGATTCTTAT
 GTGAAATTTAAAGACATTTGATTCGTCATGTAAGGATTTTCACTGTGAAGTACAATAATGCAACATCAGTGTG
 CTCAACTGCTTTATACITTTAAACAGCCATCTTAAATAAGCAACGTTTGTGAGTACTGATATGATATAATAA
 AAATATCAAGGAAAA

0978183.101501

FIGURE 181

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196
><subunit 1 of 1, 229 aa, 1 stop
><MW: 26017, pI: 4.73, NX(S/T): 0
MGDKIWLFPFVLLLLAALPPVLLPGAAGFTPSLSDSFTFTLPAGQKECFYQPMPLKASLEIEY
QVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFTSTISEKVIFFEL
ILDNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQIILLRAFEARDRN
IQESNFDVRVNFWSMVNLVVMVVSAIQVYMLKSLFEDKRKRSRT

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

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T05101" 000000

THE UNIVERSITY OF CHICAGO

CCATCCCTGAGATCTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT
CTCACCAGAGAGTGCAGACACTATGCTGCCTCCCATGGCCCTGCCAGTGTGTCTCGGATG
CTGCTTTCTGCTCAATTCTCTGTGTCAAGTTCAAGGTGAAGAAACCCAGAAGGAACTGCC
CTCTCCACGGATCAGCTGTCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT
TTTTGTCAACAAATCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGAAAAA
CTGGTGTCTGTCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCCTGGTGAGGAGCATTAG
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG
GAGATGGATGGGAGTGAGTAGCACATGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC
TCCACCATCTTAAACCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG
GAAAGATTATAACTGTGATGCAAAGTTACCTATGTCTGCAAGTTCAAGGACTAGGGGCAGGT
GGGAAGTCAGACGCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC
TCACTCTGGAGAGAGAATATTTCTCCCAAATTCAGGCTCACTGACTACCTTGTCTGATCTCTCC
TTCTTTTCCCTTTTCTTCTCACTTCAATTCAGGCTTTCTCTGTCTTCCATGCTCTTGAGATC
TCAGAGAATAAATAATAAAAAATGTTACTTTATAAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 183

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965
<subunit 1 of 1, 175 aa, 1 stop
<MW: 19330, pI: 7.25, NX(S/T): 1
MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM
DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS
TDMVNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

FIGURE 184

CCAGTCTGTGCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC
ACAGAGGAGTGGGCCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGTGGC
TGCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCGTGTCTGTGCAATACTG
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC
CTCCCACTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCCATGGCCCTATGCGGCCCA
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

0978188 101501

FIGURE 185

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP
FQGDSTVTKSCASKCKPSDVGIGQTLFVSCCNTELCNVDGAPALNSLHCGALTLLPLLRL

Important features:

Signal peptide:

amino acids 1-17

N-glycosylation site.

amino acids 46-49

09070188-101501

FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGACCCTGACTCTGCAGCCGAACCGGC
ACGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTCTCCCTCTT
GAGTCTCTCTGAGATGATGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG
TAGCGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACTCGGTTCTC
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGACGCGAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGCTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA
AGGACAAGAAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCCTCAGGATTGTGTTGTGCTA
GACACTTCTGGTCCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCAT
AGGAGAAAAGGCTCTCATGGACTAGAAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC
TTGCCGATACAGAAAGATCACCATCAAGCCAGTAATTTCTTAGGCTTCACACTGTGCAGA
GACACTAAAACCAGCTATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAACC
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT
TCCAATAACACCTTCAAAAAACCTGGAGTGTAAAGAGCTTTGTTTCTTTATGGAACCTCCCTG
TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA
AACTTTTAATTATTTTCTAAAGGTGCTGCACTGCCTATTTTCTCTGTATGTAAATTT
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACGTAAATCAAT
TCAGCTTATAGTTCTTAAAAGCATAACCCCTTTACCCATTTAATTCTAGAGTCTAGAACGA
AGGATCTCTTGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT
TTCGAAATGTACTATCTTAATGCTTAAATTATATTCCCTTTAGGCTGTGATAGTTTTTGA
AATAAAATTTAACATTTAAAAA

FIGURE 187

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA
APGILYPGGNKYQTDIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRKRRCMRH
AMCCPGNYCKNGICVSSDQNHFRGEIETITESFGNDHSTLDGYSRRTLSSKMYHTKGQEG
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKRRKGSHGLEIFQRCYCGEGLSCRIQ
KDHHQASNSSRLHTCQRH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

105101" 0010200

FIGURE 188

TGTGTTTCCCTGCAGTCAGAAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCAGCGGA
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTCTTTCTCCTTCNG
GAGTCCTTNTGAGANGATGGTTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG
GTAGCGGCGGTTTTTCGGCGGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC
AATTCCAACGNTATCAAGAACCCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT
TGCAGTCAGCGCGCGCCGGGAATCCTGTACCCGGGCGGGGAATAAGTACCAGACCATTGACA
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCAAGCTATGTGCTGCCCGGGAATTACTGCAAAAATGGAATATGTGTGTTTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGG

09973193.101501

FIGURE 189

GAGGAACCTACCGGCTACCGGCCGCGCGCTGCTAGTCGCGCGGTGGCTGCACCTCAACCAATCCCGTGGCGCGCGG
 CTGGGCGGTCCGGAAGTGGCTGCTCTCTCTGCGACGCGGTGCTTGGCTCGCCAGCGCGGGTCTCGCGCGCA
 GGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGACCCCGGATGGCAGGTATATTTTGTGGAAATGAAGAAGA
 AGTATTGAAATAGCTGTAAGACCATTCACAGATTAAATATTTTGGGACAGATTTGTGATCTTGATTCACCT
 TGAAGTAAATGTAGACAGAAGTCTCAAATTTGCATATTACATCAACTGGAAACAGCAGTGAATCTTAATGTTCC
 TTAATCAGAACTTCGATAGAAAGAGAAATGGAGGTCTGGTTAAATAAGAGTACATATATCAGAGACTTGAAGA
 GATCATTTCTCTGTTTCTGATAGTGTATATGCCATTTTAGTGGGCACAGATCAGGATTTTACAGTTTATCTGG
 AGTGCTCAAACTCGAAGCAGTAGAGAAATAGACAAGCTTTCAAGAAATTTGGCATTTGAAGTTACATCTCGATAA
 AAACCCGAAATAACCCAAATGACATGGCGATTTTAAATAATAATAGAGCATATGAAGTACTCAAGATGAAGA
 TCTACGGAAAAAGATGACAAATATGGAGAAAGGGACTTGAGGATATCAAGGTGGCCAGTATGAAGCTGGAA
 CTATTTATCGTTATGATTTTGGTATTTATGATGATGATCCTCGAAATCATAAACATTTGGAAGGAAGAATTTGATG
 TGTCTGTTAATCTGGAGAACTGTGGTTTGTAAATTTTACTCCCCAGGCTGTTCACACTGCCATGATTTAGCTCC
 CACATGGAGAGACTTTGCTAAAGAAAGTGGATGGGTACTTCGAATTTGGAGCTGTTAACTGTGGTGATGATAGAAT
 GCTTTGCGGAATGAAGGAGTCAACAGCTATCCAGTCTCTCATTTTTCGGTCTGGAATGGCCCGCAGTGAATA
 TCATGGAGACAGATCAAAGGAGAGTTTGTAGTGTTTTGCATTCAGCATGTAGAAAGTACAGTGACAGAATTTTG
 GACAGGAAATTTGTCACTCCATCAACAACTGCTTTTGTGCTGTGATTTGGCTGGCTGATCACTTTTGTTCAAA
 AGGAGAGATGTTTGTGCTTACAGACACGACTCAGGCTTAGTGCGATGTTGTTTCTCAACTCATGGATGCTAA
 AGAAATATATTTGGAAGTAATACATAATCTCCAGATTTTGAACACTACTTTCCGGAACACACTAGAGGATCGTTT
 GGCTCATCATCGGTGGCTGATTTTTCATTTTGGAAAAATGAAAAATCAAAATGATCTTGAGCTGAAAAAAT
 AAAAATCTCTATCAAAATGATCATATCAAGTTGGCAGGTTTGAAGTCTTCTCTGACACAGACATCTGTAGTAA
 TTTGTATGTTTTCAGCGCTCTATAGCAGTATTTAAAGGACAGAGAACCAAGAAATGATGAAATTCATCATGGAA
 GAGAGTTCTATATGATATACTGTGCTTTGCCAAAGAAAGTGTGAATCTCATATCTACACGCTTGGACCTCAAAA
 TTTTCTGCGCAATGACAAAGAACTGCTTGTGATTTCTTGTGCCCTGGTGTCCACATGTGAGGCTTTACT
 ACCAGAGTTACGAAAGAGCATCAAAATCTTCTTATGGTCAGCTTAAGTTTGGTACACTAGATTTGACAGTTTCA
 GGGACCTGTGAACATGTATAACATCTCAGGCTTATCCAAACACAGCAAGCTGTGATGCTTTGATTTCTATTCCG
 GTGCTCTCTGCGCAAGTCTTAATGGCCAGAAATGGAAAGAAATGGCCCGGACATTAACATGAGATGATCAAGCTGG
 CAGTATAGATTTGCCAACAGTATGATCTTTTGTGCCCGAAAGCTTCAAGATACCTCGAGATTAAGATTTT
 TCCCCCAAATCAAAATAAGCTTTATCAGTATCACAGTACAAATGGTTGGAAATGGGATGCTTTATTCCTGAGAAT
 CTGGGGTCTAGAGTTTATCTCAAGTATCCAGACATCAACACCTCAGAGCTTCAGTGAAGAAAGTTCTACAGG
 GAAAAATCATTTGGTGATTTGATTTCTATGCTCTTGGTGGGACCTTGGCCAGAAATTTGCTCAGAAATTTGAGCT
 CTGCGTAGGATGATTAAGGAGAAAGTGAAGGCTGGAAAGTAGACTGTGAGGCTTATGCTCAGACATGCCAGAA
 AGCTGGGATCAGGGCTATCCAACTGTAAAGTTTATTTCTACGAAAGAGCAAAAGAGTATTTTCAAGAAGAGCA
 GATAAATACAGAGATGAAAGCAATCGCTGCCTTAATAGTGAAGAAATTTGGAAATCTCCGGAATCAGGGCA
 GAGGAATAAGGATGAACCTTTGATTAATGTGAAGATGAAGAAAGGTTTAAAGAAATTTGATGATGACATCAG
 AAGACACCTATTAGAATTTGATATTATGATGGGAATGAATGAACATTATCTTAGACTTCAGATTGTACTGGCA
 GAATTTATCTACAGCAGCTGTGTAAAGAAAGGGTCTGCAAACTTTTCTGTAAGAGGCGGTTCTCATTTGTTTCT
 GACTTTGACAGCTATATATATGTTTACACATGAGAACAGAAATAGAGTCAATATGATTTCTTTGTTATTTGCT
 TTTAAACACCTTTTAAAAATATTAAGACGATCTTAGCTCAGAGCCATACAAAGATAGGCTGGATTCAGTCAATG
 GACCATAGATTTGCTGCTCCCTCGACGGACTTATAATGTTTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTCT
 ATCTACATAAATGTCTTAAGTTGTATAAAGTCCATTTCCCTTCAGTTTTCGGCTGACCTGAAAGAGGTAATCT
 TAGTTTGTGGTCACTGTTCTCTTAAAAATGCTATCCCTAACCATATATTTATTTGTTTAAAAACACCAT
 GATGTGGCAGAGTAAACACCTCTGTATGCTGATTAATATGAGGAGATTTCTCATTTGTTTCTTCTCTCA
 AAGGTTGAAAAATGTTTAAATTTTTCACAGCCGAGAAACAGTGCAGCAGTATATGTCACACAGTAAGTACAC
 AAATTTGAGCACAGTAAAGTGCACAAATCTGTAGTTTCTGTATCATCCAGGAAATCTGAGGGAACAAATTA
 TAGCAATTAACCTGGGATGTTAGAGTATCTCAAAATATGTTTCAAGTATTAGAGTTCTATATTTTAAAGATA
 TGTGTTCTAGTATTTCTGAAATGCTTTTACAGAAATTTTCCCACTGATAGTTGATTTTGGAGCTCAATAT
 TTTACATATTTGCTTTCTGAATTTGTTTGTACCTGTATCTTTATTTACATTTGGGTTTTCCTTCTATGTTTGG
 TTTTCTCACTCTGTCAGCTTATTTATTTCAAATAGGAAAAATTTACTTTCAGGTGTTTCTTACGTGAGCTTAT
 AATGATATGTTATTTCCAGTTTACTGTTTACTGTCTGAGGGCTGCTTTTCTAGTAAATATGACATAATA
 ACTGAAGTTTATTTTAAAGAAATCAAGTATATAAATCTAGGAAGGGATCTTTCAGTTCGTGTTGTTTGA
 CTCAAAGAAATCAAAATTTGTGAGTAACTGTAGTTGTTTAGTTATAATTCAGAGTGTACAGAAATGGTAAAAAT
 CCAATCAGTCAAAAGAGGTCAATGAATTTAAAGGCTTGCAACTTTTCAAAAAAAGAAAAA

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 105101"88105660

FIGURE 190

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439
<subunit 1 of 1, 747 aa, 1 stop
<MW: 86127, pI: 7.46, NX(S/T): 2
MGVWLNKDDYIRDLRKIILCFLIVMAILVGTQDFYSLLGVSKTASSREIRQAFKKLALKL
HPDKNPNNNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKLEDNQGGQYESWNNYYRYDFGI
YDDDEPIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC
GDDRMLCRMKGVNSYPSLFI FRSGMAPVKYHGD RSKE SLVSFAMQHVRSSTVTELWTGNFVNS
IQTAFAAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN
TLEDRLAHHRWLFFHFGKKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQP
SLAVFKGQGTKEYEIIHHGKILYDILAFAKESVNSHVTTLG PQNF PANDKEPWLVDFFAPWC
PPCRALLPELRRASNLLYGQLKFGTLDC TVHEGLCNMYNIQAYPTTVVFNQSIHEYEGHHS
AEQILEFIEDLMNPVS VVSLTPPTTFNELVTQRKHNEVWMVDFYSPWCHQCQVLMPEWKRMART
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG
FLPQVSTDLTPQTFSEKVLQGNHWVIDFYAPWCGPCQNFAPFELLARMIGKVKVAGKVDC
QAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAIALISEKLETLRNQGKRNKDEL

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGGACAGAGCAAA
GCCATGAACATCATCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCTACTTGGGA
GTCGTTGGTGAAGTTTTTTCATTCCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTGAGTGCCGAAA
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA
CATCCTTAGGACATTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAAATCATG
GCCACATCGTACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCCCTACCTCATCCCATAT
TGTTCCAGCAAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTCAGGCCTT
GGGAAAAAAGTGGTATCAAAACCTCATGTCTCTGCCAGTTTGTGTAATCTGGGTTCCACCA
AAAATCCAAGCACAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA
GATGGAATACTTACCAATAAGAAAATGATTTTTGTTCCATCGTATATCAATATCTTCTGAG
ACTACAGAAGTTTCTTCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTTCAAT
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGAATAAAATAAGTCCAGCCAGAGATG
TATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAGCTTTATTTTACATTTTT
TCAGTCTTGATAATATTAAAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA
ATTACCTGCTTCTCTGTTTCTCAAGAATATTTACGTAGTTTTTCATAGGCTGTGTTTTCTCTT
TCATGCCTCTTAAAAAAGTCTGTGCTTACATAAACATACTTAAAGGTTTTCTTTAAGATAT
TTTTATTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAGTAAATCAAAAGAGAACT
TATTTACACAGGAAGGTTTAAAGCTGTTCAAGTAGCATTTCAATCTGTAGCCATGCCACAG
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT
ATCTCAACCTGGACATATTTAAGATTGAGCATTTGAAAGATTTCCCTAGCCTCTTCTCTTT
TCATTAGCCCAAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT
AACTCTGAAGTCCACCAAAAGTGGACCTCTATATTTCTCCCTTTTATAGTCTTATAAGA
TACATTATGAAAAGGTGACCGACTCTATTTTAAATCTCAGAAATTTAAGTTTCTAGCCCATGA
TAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCAGAGATGTTTAGACAAT
TTTAGGCTCAAAAATTAAGCTAACACAGGAAAAGGAAGTGTACTGGCTATTACATAAGAA
CAATGGACCCAAGAGAAGAA

FIGURE 192

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409
<subunit 1 of 1, 300 aa, 1 stop
<MW: 33655, pI: 9.31, NX(S/T): 1
MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTFEAKRQSI
LVLWDINKRGVEETAAECKRLGVTAHAYVVDSCSNREEIYRSLNQVKKEVGDTVIVVNNAGTV
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVVFVNTGFTKNPSTRLWPVLETDEVVRSLID
GILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

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T0511T"818/660

FIGURE 193

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCAGCAGG
ATGCCCCGGTCTCTGCAGGAAGCTGAAGTGAGAGGCCCGAGAGGGGCCAGCCCCCGGGGCG
AGGATGACCAAGGCCCGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTTCATGATCCT
GCTGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGACACGTCCTTCT
CTAGGCCGCACACGGGGCCCGCTGCCACGCCGGGCCGACAGGGACAGGGAGCTCAGC
GCCGACTCCGATGTGCAGCAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA
CCTTCCCAGAAAGGAGACGGAGCAGCCGCTGCGCCGGGAGCATGGAGGAGAGCGTGAGAG
GCTACGACTGGTCCCCGCGCAGCGCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAG
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACCTCCAGCCTGGCCTTCCCCACCAAGGAGCG
CGCATTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGG
CCATCTACTGCTACGTGCCCAAGGTGGCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG
AGCGGAAGCCTGTGTCAGCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA
CGTGACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGTACGCGGAAGCTCT
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCTCTTCGTGCGCGACCCC
TTCGTGCGCCTGATCTCCGCCTTCCGAGCAAGTTGAGCTGGAGAACGAGGAGTTCTACCG
CAAGTTCGCCGTGCCATGTCTGCGGCTGTACGCCAACACACAGCCTGCCCGCCTCGGCGC
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCTTCGCCAACTTCATCCAGTACCTGCTGGAC
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC
AGCTGCTGCGACTACTCCAGGTGGACCGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG
ACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC
GAGACTGAAGCTTTCGCGTTGCTTTTCTCGCGTGCCTGGAACCTGACGCACGCGCACTCC
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC
ATTGAGTACTGTATCGATATTGTTTTTAAAGATTAATATATTTTCAGGTATTTAATACGA

09978133.10501

FIGURE 194

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112
<subunit 1 of 1, 414 aa, 1 stop
<MW: 48414, pI: 9.54, NX(S/T): 4
MTKARLFLWLVLGSGVFMILLIIIVYWDSAGAAHFYLHTSFSRPHGTGPPLPTPGPDRDRELT
DSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESEVRGYDWSPRDARRSPDQGRQQAER
RSVLRGFCANSSLAFTKERAFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLS
GSLLRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF
VRLISAFRSKFELNEEFYRKFAVPMRLRYANHTSLPASAREAFRAGLKVSFANFIQYLLDP
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLDDEAAQLLQLLQVDRQLRFPSPSYRNT
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

Important features:

Signal peptide:

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

FIGURE 195

TCGGGCCAGAATTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA
AAGAGGCCCAGAGTAGAGAGAGAGAGACCGACGTACACGGGATGCTACGGGAACGCGCT
ATGCCGGGAAGGTGGTGGTCGTGACCGGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC
GCCTTCGTGAACAGCGGGGCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGC
CCTGGAGCAGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG
TGAAGACCCCTGGTTTCTGAGACCATCCGCCGATTGGCCGCCCTGGATTGTGTTGTCAACAAC
GCTGGCCACCCACCCACCCCCACAGAGGCCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCTTACCTGCGGA
AGAGTCAAGGGAATGTCAACAATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCAGGCA
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCAGGAAACATCTGGACCCCGCTGTGGG
AGGAGCTGGCAGCCTTAATGCCAGACCCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCCAG
CCACTGGGCCGCATGGGCCAGCCCGCTGAGGTGCGGGCTGCGGCAGTGTTCTGGCCCTCCGA
AGCCAACCTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGACAGAGCTGGGGTACGGGT
GCAAGGCCAGTCGGAGCACCCCGTGACGCCCCGATATCCCTTCTGATTTCTCTCATTT
CTACTTGGGGCCCCCTTCTAGGACTCTCCACCCCAAACCTCCAACCTGTATCAGATGCAGC
CCCCAAGCCCTTAGACTCTAAGCCAGTTAGCAAGGTGCCGGGTACCCCTGCAGGTTCCCAT
AAAAACGATTTGCAGCC

00078163.101501

Figure 1

<subunit 1 of 1, 270 aa, 1 stop

MATGTRYAGKVVVVTTGGRGIGAGIVRAFNVSGARVVICDKDESGGRALEQELPGA VFILCD
VTQEDDVTKLVSETIRFRGLRDCVUNNAGHPPPPRPEETSAGGFQRLLENLLGTYTLTKL
ALPYLRKSSQGNVINISSLVGAIGQAQAVPYVATKGAVTAMTKALALDES PYGVRVNCISPGN
IWTPLWHEELAALMPDPDPATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTGG
AELGYGCKASRSTPVDADIPDS

N-glycosylation site.

amino acids 138-141

amino acids 10-22, 81-91, 134-171 and 176-185

amino acids 10-22, 81-91, 134-171 and 176-185

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATTGGACTGGCCTCAACAACCTG
CTGTTTCTTCTTACCATTTCATCTTCTCTGGGGCTGGGCCAGCCAGGAGCCCCAAAAGCAA
GAGGAAGGGGCAGGGCGGGCTGGGCCCTTGGCCCTTGGCCCTCACCAGGTGCCACTGGACC
TGGTGTACCGGATGAAACCGTATGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG
GTGGCCACAGCTGAGGAACAGCTCAGAGCTGGCCAGAGAAAGTGTGAGGTCAACTTGCAGCT
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCACAGCC
GTATCCCGTGGACCTGCCGGAGGACCGGTGCCCTGTGTCTGGGCTGTGTGAACCCCTTCACC
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCCGTGTTCAGCCAGGTTCTCTGTGCGCCGCCG
CCTCTGCCCCCACCAGCCCCGCAAGGGCCTTGCCGCCAGCGCGAGTCATGGAGACCATCG
CTGTGGGCTGCACCTGCATCTTCTGAATCACCTGGCCAGAAGCCAGGCCAGAGCCCGAGA
CCATCTCTCTTGACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGA
GCAAG

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Important features:

amino acids 1-20

amino acids 75-78

amino acids 96-180.

amino acids 96-180.

FIGURE 199

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGGCTCTCCGCTTCCCTTGAAAAACCCGGCGGG
CGAGCGAGGCTGCGGGGCCGGCGCTGCCCTTCCCCCACTCCCCGCCGAGAAGCCTCGCTCG
GCGCCCAA**CAT**GGCGGGTGGGCGCTGCGGCCCGCAGCTAAACGGCGCTCCTGGCCGCTGGAT
CGCGGCTGTGGCGCGAGCGCAGGCCCCGAGGAGGCCGCGCTGCCCGCGGAGCAGAGCCGGG
TCCAGCCCATGACCCGCTCAA**CT**GGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT
TACGCCCCATGGTGTCCATCCTGCCAGCAGACTGATTCAGAAATGGGAGGCTTTTGCAAAGAA
TGGTGAAT**ACT**TCAGATCAGTGTGGGGAGGCTAGATGTCA**TT**CAAGAAC**CC**AGGTTTGAGATG
GCCGCTTCTTTGTCA**CACT**CTCCAGCATT**TTTT**TCATGCAAAGGATGGGATATTCCGCGGT
TATCGTGGCC**CAG**GAATCTTCGAAGACCTGCAGAA**TT**TATATCTTAGAGAAGAAATGGCAATC
AGTCGAGCCTCTGACTGGCTGGAAATCCCGAGCTTCTCTAACGATGTCTGGAATGGCTGGTC
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCA**CACT**ATTTACAGTGACTCTTGGAAT
CCTGCTTGGTGTTCTTATGTGTTTTCGT**CAT**AGCCACCTTGGT**TTTT**TGGCCTTTTATATGGG
TCTGGTCTTGGTGGTAAATCAGAA**TG**TTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG
GAGGAAAAAGATGATTCAAATGAAGAAGAAAA**CA**AGACAGCCTTGTAGATGATGAAGAAGA
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGACAACTTGGCTG
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGCCCCAGGAGAGGACGGTGTG
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCTTGCCAGC
TGACACAGAGGTGGTGAAGACTCCTTGAGGCAGCGTAAAGTCAGCATGCTGACAAGGGAC
TG**TAG**ATTTAATGATGCGT**TTTT**TCAAGAATACACACCAAA**CA**ATATGTAGCTTCCCTTTGG
CCTGCAGTTTGTACCAATCCTTAATTTTCTGAATGAGCAAGCTTCTCTTAAAGATGCT
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT
GACAA**T**CAGGATATAGAAAA**CA**ACCGTAGTGTGGGATCTGTTTGGAGACTGGGATGGGAA
CAAGTTCA**TTT**ACTTAGGGGTCAGAGAGTCTCGAC**CAG**AGGAGGCCAT**CC**CAGTCCTAATC
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAATGAAGCCAAGCAGGAGGCCTTGGCT
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGATCCTTTTCTTGTGAAGTATTTAT
TTTTGTCAAAT**TG**CAGGAACATCAGGCAC**CA**CAGTGCA**TG**AAAAATCTTT**CA**CAGCTAGAA
ATTGAAGGGCCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCAGCCCTCTGAATCTCCTG
TGCTATGTTTATTTCTTACCTTTAATTTTCCAGACTTTCCACATGGGCATT**CAG**CTCT
CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTT**CAT**GAAC
TGTGTTTGTTCATTTCTGACCTAAGGGGTTTAGATAATCAGTAAC**CA**TAA**CC**CTGAAGCTGT
GACTGCCAAACATCTCAA**TG**AAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGAT
TTACAGACAGATTA**AAAA**AAATGTTTTGTCCAAATATAGTTGTTGTTGATTTT**TTTT**
AAGTTTCTAAGCAATATTTTCAAGCCAGAAGTCTCTAAGTCTTGCCAGTACAAGGTAGT
CTTGGAAGAAAAGTTGAATCTGTTTGT**TTTT**CTCAAGGGGTTCCCTGGGTCTTGAAC
TACTTTAATAATA**CA**TAAAA**AC**CACTTCTGATTTTCTT**CAG**TGATGCTTTTGGTGA**AA**
GAATTAATGA**CT**CCAGTCAAGTGAAGTGAAGATTTGATTTGTTCCATCTTCTGTAATC
TTC**CA**AGAATATATCTTTGTAAATCTCTCA**TA**CTCAATCTCA**TG**TAAGTAC**CC**AGGGAG
GCTAATTTCTTT

FIGURE 200

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433
<subunit 1 of 1, 349 aa, 1 stop
<MW: 38952, pI: 4.34, NX(S/T): 1
MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMASNWTLVMEGEWMLKFYAP
WCPSCQQQTDSEWEAFKNGEILQISVGKVDVIEPGLSGRFFVTTLPAFFHAKDGIFFRRYRG
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW
CSYVFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSESEQNRRSEEAHRAEQLDAAEEK
DDSNEEENKDSLVDDEEKEDLGDEDEAEEDNLAAGVDEERSEANDQGPPGEDGVTRE
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSHADKGL

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

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FIGURE 201

ATCTGGTTGAACTACTTAAAGCTTAATTTGTTTAACTCCGGTAAGTACCTAGCCACATGATT
 TGACTCAGAGATTCTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC
 CAAATGCTATATCTAATTACAGGGGCTCTCAAGAACAAATGGGAATATCATCTGATTTAGAAAAAT
 TTGGATGAGATGGATATATCTCAATTACACTTCGACTCTCAAAGCAATACAGGATAGCTGT
 TGTTCACAGAAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCTGTAATTTTGG
 GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGGTTCTTTCC
 AGCCCTTGTCCTCCTAATTGGATTATATATGAGAAGAGCTGTTATCTATTACAGCATGTCACT
 AAATTCCTGGGATGGAAGTAAAGACAAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG
 ACAGCTCAAATGAATTTGGGATTTATAGTAAAAACAAGTGTCTTCCCAACCTGATAATTCATTT
 TGGATAGGCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT
 CTCTTCTAATCTAATTTTTCAGATCAGAACCACAGCTACCCAGAAAAACCCTATCTCCAAATTGTG
 TATGGATTACAGTGTCACTCATTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT
 GAGAAGAAGTTTTCAATGTAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTA
 AGGAGGACAGAAAAACAGAAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAAATGCGAGAAAATG
 TTTAGAGAGCTTGGCCAACTGTAATCTTAACCAAGAAATGAAAGGGGAGAGGCTGTGATTTCCT
 GTATTTGTGCACTTACAGGTAGGCTAGTATTATTTTCTAGTTAGTAGATCCCTGACATCTGG
 AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTTTATTTTATTTTATTTTGGAGATAGGGTCT
 CACTTTGTATTACCAGGCTGGAGTGCAGTGGCAACAATCTCGACTCACTGCAGCTATCTCTCGC
 CTCAGCCCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTGGTG
 TTTTGTGTAGAGACTGGGTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAG
 TGATCTGCCCGCTTGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCACACCTGGC
 CCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTACCTTGGGTAAAGCCATAAGCGA
 ATCTTAATTTCTGGCTCTATCAGAGTTGTTTTCATGCTCAACAATGCCATTGAAGTGCACGGT
 GTGTGCGCAGATTTGACCCCTCAACTTCTAGCAGTATATCAGTTATGAATGAGGTTGAAAT
 ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAAATCTTCACCACAGTCAGAGCAATTTT
 ATTTATTTTTCATCAGTATGATCATAATTTATGATTATCATCTTAGTAAAAAGCAGGAACTCCTA
 CTTTTCTTTTATCAATTAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT
 TTTTTTTTTTTTTTTTTTTTGGACAGAGTTTCGCTCTTGTGTGCCAGGCTGGAGTGCAACGG
 CACGATCTCGGCTCACCGCAACCTCCGCCCTTGGGTTCTAAGCAATTTCTCTGCCCTCAGCCT
 CCCAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTGTATG
 AGAGACAGGGTTTCTCCATGTCTGGTCAAGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGC
 CTGCCTCGGCCCTCCCAAGTGCTGGGATTAAGGCGTGAGCCACTGCACCCAGCCTAGAATCT
 TGTATAATATGTAATGTAGGGAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTTAAATACA
 AAAATACATAAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA
 ACAAGTATTAACATTTTGGAAATATGTTTTATTTAGTTTGTGATGTACTGTTTTTACAATTTTT
 ACCATTTTTTTTCAGTAATTTACTGTAAATGGTATTATTGGAATGAAACTATATTTTCTCATG
 TGCTGATTTGTCTTATTTTTTTCATACTTTCCCACTGGTGCTATTTTATTTCCAATGGATA
 TTTCTGTATTACTAGGGAGGCATTTACAGTCTCTAATGTTGATTAAATATGTGAAAAGAAAT
 TGTACCAATTTTACTAAATATGCAAGTTTAAATGGATGATTTTATGTTATGTGGATTTCAT
 TTTCAATAAAAAAACTCTTATCAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

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<subunit 1 of 1, 201 aa, 1 stop

MEYHPDLENLDEDDGYQLHFDQSQSNTRIAVSEKSGCAASPWRLIAVLILGILCLVLIVIAV
VLGTMGVLVSSPCPPNWIIEYKSCYLFMSLSNSWDGSKRQCWQLGSNLLKIDSSNELGFIQVKQ
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL
CSVPSYSICEKKFSM

Type II transmembrane domain:

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

FIGURE 204

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MTPQSLQLQTTLFLLSLLFLVQGAHGRGHREDFRFCSQRNQTHRSSSLHYKFTPDLRISIENSE
EALT VHAPFPAAHPASRSFPDPGRGLYHFCLYWNRHAGRLHLLYGKRD FLLSDKASSLLCFQH
QEESLAQGPPLLATSVTSWWSQPONISLPSAASF TFSFHSPPHTAAHNASVDMCELKRD LQLL
SQFLKHPQKASRRPSAAPASQQLQSLESKLT SVRFMGDMVSFEEDRINATVWKLQPTAGLQD
LHIHSRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
KVLGIVVQNTKVANLTEPVVLT FQHQLQPKNVTLCQVFVVEDPTLSSPGHWSSAGCETVRRE
TQTSFCFNHLTYFAVLMVSSVEVD AVHKHYLSLLSYVGCVVSA LACLV TIAAYLCSRVP LPC
RRKPRDYTIKVHMNLLLA VFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLE
GYNLYRLVVEVF GTYVPVGYLLKLSAMGWGFPI FLVTLVALVDVDNYGPIILAVHRTPEGVIY
PSMCWIRDSLVSYITNLGLFSLVFLFNMA MLATMVVQILRLRPHTQKWSHVL TLLGLSLVLG
LPWALIFFSFASGTFQLVVLYLFSIITSFQGFLIFIWYSMRLQARGGPSPLKSNSDSARLP
ISSGSTSSSRI

Important features:

Signal peptide:

amino acids 1-25

Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657

Microbodies C-terminal targeting signal.

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344

G-protein coupled receptors family 2 proteins

amino acids 475-504

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FIGURE 205

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCCTTCCAGGTTGCCCTGCCTTGCGA
GGAANNCNTCGGGACTACACCNCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCCTGCTG
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCCTTTCCTGGATGGGCCTCGAGGGG
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA
GCTGAGCGCCATGGGCTGGGGCTTCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG
TGGACAACCTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCT
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT
GGTGTTCCTGTTCAACATGG

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FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTCAGGTCACAGGTTTGTCTTGA
TCCTTTTCAAAACTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTGGATGGGATTTATGTGGAACTACCT
GCGATTCTCTGCTGCGAGAGCAGGCTCGGCGCTTCCACCCAGTGCAGCCTTCCCCTGGCGGTGGTGAAGAGAC
TCGGGAGTGCCTGCTTCCAAAGTGCCCGCGTGGTGGCTCTCACCCAGTCAAGCCAAATGAGCCTCTTCGGGC
TTCCTCTGTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGGATAGTAAATCC
AGTTTTCAGCAACAAGGAACAGAACGGAGTACAAGATCCCTACAGATGAGAGATTTATTAATCTGATCTACTAATG
GAAGTATTACAGCCCAAGGTTTCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG
AGGAAATATGTATGGATACAACCTTACGTTTGATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGT
ATGATTTTGTAGAAATGAGGAACCCAGTGTGGAATATATATAGGCGCTGGTGGTCTCTGGTCTGATCTGACAG
GAAAAAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTCTCTGTAACAGGGT
TCTGCATCCACTACAACATTTGTCATGCCCAATTCACAGAAGCTGTGAGTCCCTCAGTGCTACCCCTTCAGCTT
TGCCACTGGACCTGCTTAATAATGCTATACCTTGCTTTAGTACCTTGGAGAACCTTATTGATATCTTGAACAG
ACAGATGGCAGTTGGACTTAGAAGATCTATAGGCCAACTTGGCAACTCTTGGCAAGGCTTTGTTTTTGGAA
GAAAAATCCAGAGTGGTGGATCTGAACCTTCTACAGAGAGGGTAAGATTATACAGCTGCACACCTCGTAACCTCT
CAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTG
GTGGGAACTGTGCTGTGTCTCCACAAATGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC
ACGAGGTCCTTCAGTTGAGACCAAGACCGGTGTGAGGGATGACAAATCACTACCAGCGTGGCCCTGGAGC
ACCATGAGGAGTGTGACTGTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGATCACACCAGCAGCTCTTGCCCA
GAGCTGTGTCAGTGCACTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCTCTAATCTCAGTTGTTTGTCT
TCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTTCTGAAAGAGGAGACATCAACAGAAATTAGGAGTTGTGCA
ACAGCTCTTTTGAAGAGGAGGCTAAAGGACAGGAGAAAAAGGTTCTCAATCGTGGAAAGAAAAATTAAGTTGTAT
TAAATAGATCAACAGCTAGTTTTCAGAGTTACCATGTACGTATTCACATAGCTGGTCTGTATTTTCAGTTCTTCT
GATACGGCTTAGGGTAATGTGAGTACAGGAAAAAACTGTGCAAGTGAGCAGCACTGATTCCGTTGCTTGCCTTAAC
TCTAAAGCTCCATGTCTGGGCTAAATATCGTATAAAATCTGGATTTTCTTTTCTTTTGTCTCATTTACAT
ATGTAAACAGGAACATCTATGTACTACAAACCTGGTTTTTAAAGGAACATGTGTCTATGAATTAACATTTGT
GTCTGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAATTTCTGCAATTTAGAGAGAGAACTACA
TTCATGGTTTGGAAAGAGATAAACCTGAAAAAGAGAGTGGCTTATCTTCACTTTATCGATAAGCTGATTTATTG
TTTCATTTGTACATTTTATATTTCTCTTTTGACATTTAACTGTTGGCTTTTCTAATCTTGTAAATATATCT
ATTTTACCAAAGGTATTTAATATTTCTTTTATGACAACTTAGATCAACTATTTTAGCTTGGTAAATTTTCT
AAACACAATTTGTATAGCCAGAGAGCAAAAGATGATATAAAATATGTGTCTGACAAAAATACATGTATTTCA
TTCCTGATGTGTGCTAGAGTTAGATTTAATCTGCATTTAAAAAACTGAATTGAATAGAATTTGGTAAGTGCAAA
GACTTTTGAATAATTAATATCATATCTTCCATTTCTGTATTTGGAGATGAAATTAAGAACCACTTATGA
AAGTAGACATTCAGATCAGCCTACTAACCCTATCTTTTGGGAAATCTGAGCTAGGACCTCAGAAAAACAT
AAGCACCTTTGAAAGAGACTGGCAGCTTCTGATAAAGCGTGTGTGTGTGTCAGTGGGAACACATCTTATTA
TTGTGATGTGTGTTTTATTATCTTAACTCTGTATTCATACACITTTGATATAATACATGGATATTTTATGTACA
GAGATATGTCCTTAACAGTTTCACTTATTTACTCTGCGAAATTTAAAGAAAACTAGTAAAAATTTTGTCTGT
AAAACTGCTTAATATNGTCCCTAGGTATGTGTGACTATTTGAATCAAAATGTATTGAATCATCAATTAAGGA
ATGTGCTATTTTGGGAGAAAAATTAAGAAAAAAGGTTTAGGGATACAGGGTAAATGCGGCC

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FIGURE 207

MSLFGLLLLSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR
FPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLL
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKSRVVDLNLLEEVRLY
SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNEQCQVPSKVTKKYHEVLQ
LRPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG

Signal sequence:

amino acids 1-14

U59/65/66/67/68/69/70/71/72/73/74/75/76/77/78/79/80/81/82/83/84/85/86/87/88/89/90/91/92/93/94/95/96/97/98/99/100

FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACAGGACCTCTACATTTCCATTTTGGGAAGA
 AGACTAAAAATGGTGTTCCTAATTTGGGACACTGAAGAGACAAATCTTATCCTTTTAAACATAATCCTAATTTCC
 AAATCCTCTGGGGCTAGATGGTTTCTCTAAAACCTCTGCCTCTGATGTCACTCTGGATGTCTTCAAAAGAACCATGTG
 ATCTGGGACTGCACAGACAAGCATTTGACAGAAATTCCTGGAGGTATCCCCAGAACACCCGAACTCACCCTC
 ACCATTAAACACATACAGGACATCTCCCCAGCGTCTTTCACAGACTGGACCATTCTGGTAGAGATCGATTTTCAGA
 TGCACCTGTGTACCTATTCCCTGGGGTCAAAAAACACATGTGCATCAGAGGCTCGAGATTAAACCCAGAAAGC
 TTTAGTGGATCACTTATTAAAAATCCCTTTACCTGGATGGAAACCACTACTAGAGATACCCGAGGGCTCCCG
 CCTAGCTTACAGCTCTTCAGCCTTGAGGCCAACCAATCTTTTCCATCAGAAAAGAGATCTTACAGAACTGGCC
 AACATAGAAATACTCTACTCTGGGCCAAAACCTGTTATTATCGAATCTTGTATTGTTCATATTCAATAGAGAA
 GATGCTCTCTAACTTACAGAAAGTAAAAAGTGCTCTCCTGAAAGATAACAATGTCAACAGCGCTCCCTACTGTT
 TTGCCATCTACTTTTACAGAACTATATCTCTACAAACAACTGATTGCAAAAAATCCAAGAAAGATGATTTTAAATAC
 CTCAACCAATTACAAATTTCTGACCTAAGTGGAAATGGCCCTCGTTGTATAATGCCCAATTTCCCTTGTGGCGCG
 TGTAAAAAATAATTTCTCCCTACAGATCCCTGTAAATGCTTTTGATGCGCTGACAGAAATAAAAAGTTTACGCTTA
 CACAGTAATCTCTTCAGCATGTGCCCCCAAGATGGTTTAAAGACATCAACAACTCCAGGAACTGGATCTGTCC
 CAAAACCTCTTGGCCAAAGAAATTTGGGGATGCTAAATTTCTGATTTTCTCCCGACCTCATCCAATTTGGATCTG
 TCTTTCAATTTTGAACCTCAGGTCTATCTGTGCATCTATGAATCTATCAAGCATTTTCTTCACTGAAAAGCCTG
 AAAAATCTGCGGATCAGAGGATATGCTTTTAAAGAGTTGAAAAGCTTTAACTCTGCCCATTAACATAATCTTCAA
 AATCTTGAAGTTCTTGATCTGGCACTAATCTTATAAAAAATGTCAACCTCAGCATGTTTAAACAAATTTAAAGA
 CTGAAAGTCTAGATCTTTTCAGTGAATAAAATATCACTTCAGGAGATTCAAGTGAAGTTGGCTCTTGCTCAAT
 GCCAGAACTCTGTAGAAAGTTATGAACCCAGGTCCTGGAAACAAATACATATTTCAGATATGATAAGTATGCA
 AGGAGTTGCAGATTCAAAAAACAAAGAGGCTCTTTTCATGTCTGTTAATGAAAGCTGTACAAGTATGGGCAGACC
 TTGGATCTAAGTAAAAATAGTATATTTTTTGTCAAGTCTCTGATTTTCAGCATCTTTCTTCTCATAAGTCCGTG
 AATCTGTGAGGAAATCTCATTAGCCAACTCTTAATGGCAGTGAATCCAACTTTAGCAGAGCTGAGATATTTG
 GACTTCTCCAACCAACCGGCTGATTACTCCATCAACAGCATTGTGAAGAGCTTCAACAACTGGAGAGTCTGGAT
 ATAAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAACTTTACCAAGAACCTAAAGGTT
 CTGCAGAACTGATGATGAACGACAAATGACATCTCTCTCCACAGCAGGAGCACTGAGAGATGAGTCTCTTAGA
 ACTCTGGAATTCAGAGGAAATCACTTAGATGTTTTATGAGAGAGAGGTCAAACTGATACAGATCTTACAATTTCAAG
 AATCTGCTAAAAATAGAGGAATTAGACATCTTAAAAATTCCTAAGTTCTTGCTCTTGAGTTTGTGATGTT
 ATGCTCTCAAAATCTAAAAGATCTCTCTTTGGCCAAAAATGGGCTCAAACTCTTCAGTTGGAGAGAACTCAGGTG
 CTAAGAGCTCCGAAATCTTTGGACCTCAGCCACAACTCACTGACCACTGTCCTTGAGAGATTTATCCACTCTCC
 AGAAGCTCAGAAATCTGATCTCTTAAAGATATCAAACTCAGGAGCTGACGAAATTTTCTACAAGATGCTTCC
 CAGTTGCGATATCTGATCTCAGCTCAAAATAAAATCAGATGATCAAAAGACACAGCTTCCACAGAAATGTCCTC
 AACCAATCTGAAGATGTGTTCTTTGTCATCAATCGGTTTCTGTGCACTGTGATGTGATGTTGCTCTGGTGG
 GTTAAACCATACGAGAGTGACTATCTTACCTGGCCACAGATGTGACTTGTGTGGGCGCAGGAGCACACAAAGGC
 CAAAGTGTGATCTCTCCCTGAGTCTGTACACCTGTGATGTAGATCTGACTAACTGATCTGTTCTCACTTTCCATA
 TCTGTATCTCTCTTTCTCATGTGATGATGACAGCAAGTCACTTATTTCTGGGATGTGGGTATATTTACCAT
 TTTGTGTAAGGCCAAGATAAAGGGATCAGCGTCTAATATCACCAGACTGTGCTATGATGCTTTTATTGTGTAT
 GACCTATAAGACCAGCTGTGACCGAGTGGGTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCGAAGAGAGAAA
 CATTTTAAATTTATGCTCGAGGAAAGGAGCTGGTTACCGAGGCGACCCAGTTCTGGAAGAACTTTCCACAGAGCA
 CAGCTTAGCAAAAGGACAGTGTCTTGTGATGACAGCAAGTATGCAAGAGCTGAAAATTTTAAAGATGATCTTAC
 TTTGTCCCATCAGAGGCTCATGGATGAAAAGTTGATGTGATCTGTGATATTCTTGAGAGCCCTTTCAAGAG
 TCCAAGTTCTCAGCTCCGAAAAGGCTCTGTGGAGTTCTGTCTTGAGTGGCCCAACAAACCCGACAGCTCAC
 CACTACTCTCTGGCAGCTCTAAAGAGCGCCCTGGCCACAGACAATCATGTGGCCTATGATCAGGTGTTCAAGGAA
 CCGGTCTAGCCCTCTTTGCAAAACCAACTGCCTAGTTTACCAAGGAGGCTGGC

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FIGURE 209

MVFPMWTLKRQILILFNIIISKLLGARWFPKTLPCDVTLDVDPKNHVIVDCTDKHLTEIPGG
IPTNTTNLTILTINHDPDISPASFHRLDHLVEIDFRCNCVPIPLGSKNNMCIKRLQIKPRSFS
GLTYLKSLLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLQNCYYR
NPCYVSYISIEKDAFLNLTCLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNL
NQLQILDLSGNCPRCYNAPFCAPCKNNSPLQIPVNAFDALTELKVLRHLSNSLQHVPPRWF
KNINKLQELDLSONFLAKEIGDAKFLHFLPSLIQLDLSFNELQVYRASMNLSQAFSSLSKL
KILIRIGYVFKELKSFNLSPLHNLQNLEVDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGO
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH
STAFBELHKLLEVDISSNSHYFQSEGITHTMLNFTKNLKVQLKMMNDNDISSSTSRTMESES
LRTLFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPNKLKNSL
AKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQ
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTDAVWVFWVWNHTEVTIP
YLATDVTCVGPAGAHKGQSVISLDLYTCELDLTNLILFSLISISVSLFLMVMMTASHLYFWDVW
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPVTEWVLAEVLAKLEDPREKHFNLCLEE
RDWLPQGQVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLE
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 840-860

09070150.101507

FIGURE 210

GGGTACCATTCTGCGCTGCTGCAAGTTACGGAATGAAAAATAGAACAAACAGAAACATGGAAAAACATGTTCCCTTC
 AGTCGTCAATGCTGACCTGCTCAATTTTCTCTGCTAAATATCTGGTTCGTGAGTTATGCGCCGAAGAAAAATTTTCTTA
 GAAGCTATCTCTTGATAGAGAAAAAGCAAAATGACTCAGTTATTGACAGAGTCAGCAATCTGCTCACTACAGAGAG
 TTCGCCAAACGCTGGGCAAAATATGTCAGACAACTAGACCTGCTGATAATTTTCATCACACATACAGGAATGAAT
 CATTTTCAAGGGCTGCAAAATCTCACTAAAAATAATCTAAACCACAACCCCAATGTACAGCACCAGAACCGGAAATC
 CCGGTATACAAATCAATAGGCTTGAATATCAGACAGGGGCATTCCTCAACCTTAAAAAACCTAAGGGAGTTACTGCT
 TTGAAGACCAACAGTATCCCAAAATACCTCTGGTTTGGCAGAGTCTTTGACAGAACTTAGTCTGAATTTCAAAACA
 ATATATAACAACTAACTAAAGAGGGGCATTTCAAGACTTATAAATCTGAAAAATCTCTATTGGSCCTGGAACTGCT
 ATTTTAACAAATTTGGGAGAAAACTAACTAGAGAGTGGAGTATTGAAACGCTGACAAATTTGGAGTTGCTGCTAT
 CACATCTCTTCAATCTCTTTACACAGTCCCAACCAATGCAAGCTCCCTACGCAAACTCTTTTCTGAGCAACA
 CCCAGATCAAAATCATTTAGTGAAGAAGATTTCAGGGGATTGATAAATTTAAACATTATAGATTTAAGCGGGAACT
 GTCCGAGGTGCTTCAATGCCCACTTTCCATGCGTGCTTGTGATGGTGGTCTCAATTAATATAGATCGTTTTTG
 CTTTTCAAACTTGACCACTCTCGATACCTTAAACCTCTCTAGCACTTCCCTCAGGAAGATTAAATGCTGCTGGT
 TTAATAATATGCTCTATCTGAAGGTGCTGGATCTTGAATTCACATTTTAGTGGGAGAAATAGTCTCTGCGGCAT
 TTTTAAACGATGCTGCCCGCTTAGAAATACTTGACTTGTCTTTAACTATATAAAGGGGAGTTATCCACAGCAT
 TTAATATTCTCAGAAATCTCTTAAACTTTTGTCTCTACGGGCATTCGATTTAAGAGGTTATGCTTCCAGGAAC
 TCAGAGAAGATGATTTCCAGCCCTGATGACGCTTCCAACTTATCGACTATCAACTTGGGTATTAATTTTATTA
 AGCAAAATCGATTTCAAATCTTTCAAATAATCTCCAATCTGGAAATATTACTTGTGAGAAACAGAAATATCAC
 CGTTGGTAAAGATACCCCGCAGAGTTATGCAAAATAGTCTCTTTTCAACGTATATCCGGAACGACGCTCAA
 CAGATTTGAGTTTGAACCCACATTCGAACTTTTATCATTTTCCACCGCTCTTTAATTAAGCCAAATGTGCTGCT
 ATGGAAGAGCCTTAGATTTAAGCCTCAACAGTATTTTCTTCAATGGGCCAAACCAATTTGAAAAATCTTCTGAC
 TTGCTGTTTGAATTTGTCGCAAAATAGCAATGCTCAAGTGTTAAGTGAACATGAAATTTTCAAGCATCTGCTCAT
 TCAAATATTAAAGTTTGTACCAAACTAGACTAGACTTTGATAAGCTGATGCTTACTGAATTTGCTGAGTGG
 AAGTCTAGATCTCAGCATTAATTTACACATTTTCAGAAATGACAGGCGTAAACATCATCTAGAAATTTATTCAAA
 ATTTTCAAAATCTCAAAATTTTAAACTTGGAGCCAAACAACTATTTACTTTTAAACAGATAGATTAACCTGGAAA
 GCAAGTCCCTGGTGAAGATTGATTTTCAAGTGGCAATCGCCTTGACATTTTGTGGAATGATGACCAACAGGTAT
 TCTCAATTTTCAAAGTCTCAAGAACTGACACGCTCGAATTTATCCCTTAAATAGGCTGAAGCATATCCCAATG
 AAGCATTCCTTAAATTTGGCAGGAGTCTCACTGAACATATATAATGATAATGTTAAAGTTTTTTAACTGGA
 CATTACTCCAGCTGTTCTCGTCTGAGTTGCTTGACTTACGTGGAAACCAACTACTCTTTTAACTAGATGCC
 TATCTGACTTTACATCTTCCCTTGGGACACTGCTGCTGAGTCATAACAGGATTCGCCACCTACCTCTGCTCTTC
 TTTCTGAAGTCACTAGTCTGAAGCACTCGATTTAAGTTCCTAATCTCGCTAAAAACATACACAAATCCGCACTTG
 AAATAGAGCCACCAAAATTTCTATGTTGGAACTACACGGAAACCTCTTGAAGTCACTCTGACATTTGGAG
 ATTTCCGAAGATGGATGGATGAACATCTGAAATGCAAAATTTCCGACACTGGTAGATGCTATTGTCGCGAGTCTG
 GGGATCAAAGAGGGAAGATTTGTGAAGTCTGGAGCTAAACACTTGTGTTTCAAGATGTCATGCTGAGTATAT
 TTTTCTTCAAGTCTTTATACCAACCAATGGTTATGTTGGCTGCCCTGGCTCACCATTGTTTCTAGGGATGTTT
 GTTTATATATAATGTGTGTTTAGCTAAAGTAAAGGCTACAGGTTCTTTCCCACTGCTCAATCTTTCTATGAT
 CTTACATTTCTTATGACCAAGAGTGCTCTGTACTGACTGGGTGATAAATAGAGTGGCTACCCACTTGAAG
 AGAGCCGAGACAAAAAGCTTCTCTTGTGTAGAGGAGGAGGTTGGGACCCGGGATTTGGCCATCATGCAACCT
 TCATGACAGACATCAACCAAGAGCAAGAAACAGTATTTGTTTAAACAAAAAATATGCAAAAGACTGGAACTTTA
 AAACAGCTTTTACTTGGCTTTGACAGGCTAATGGATGAGAACATGGATATATTTATCTGTTGAAGC
 CAGTGTATGACAGATCTCAGTATTTAGGCTACCGCGAGGATCTGTAAGAGCTCCATCTCTCAGTGGCCTGACA
 ACCGTAAGGAGCAAGAGCTTGTGTTGGCAAACTCTGAGAAATGTGGTCTTGACTGAAATGATTAATTTATCTGAGC
 ATATATGTATGCTGATCCCATTAAGCAATACTAATGACGTTAAGTATGATTTTCCGCGCATTAATTAAGATGCAAG
 GAATGACATTTTCTGATTTAGTTATCTTATGCTATGTAAACAAATTTACCAAACTTAGTGGTTTAAAGCAACACA
 TTTGCTGAGCCACAGTTTTTGAAGGTCAGGAGTCCAGGCCAGCAATACCTGGGTCTCTGCTCAGGTTGCTCAG
 AGGCTGACATGTAGGTGTTTCAACAGACATAGGCATCACTGGGTCACTATGTGGTTGTTTCTGTTGATTC
 ATTTCTCTGCGGCTATTTGGCCAAAGGCTATCTCATGTAAAGCATGCGAGCTCTCCCAACAGGCACTGCTCT
 ATCAGAGCTGACAAAAAGAGAGGTTGCTAGCAAGATGAAGTCAAACTTTGTTAATCAAAATGATCAAAAGGAT
 ATCTCATCAGCTTTGGCCATTTCTATTGTTAGAAAGTAAACCAAGTCCCAAGCTCATGGAGTGAACCC
 TCACTGACGGAACAGCTGAAGACCAAGATGGTGAAGTCTGATGCTTCAAGTCAAGTCACTCAATTTTCCCT
 TGAATGCTGCTGAGGATGGCTGCTATCTTGATGATAGATTGTGAATATCAGGAGAGCAGGATCATGCTGGAGC
 ATCTTAGCAGTCTCACTCAACATCTCTTTTCAATATCTAAGAACTTTTGGCTGAGTCAATGGTCTTAAT
 TTAAGCTGTGTTTATATTTATCATATCTATGGCTACATGGTTATATTTATGCTGTGGTGTGCTGCTGGTTTAT
 TTAAGTGTGCTTTTAAACAATTTTGTGCTAACTTTGACTTCAAGGTTTGAAGTGCATTTAAGACATGAGATGG
 ATAGCTTTTAAAGCATCTTTTACTTCTTACCATTTTTAAAGTATGACAGTAAATTCGAGCTTTTGGTCTATA
 TGTGTTAATGCCATTGCTGTAATCTTAAATGAATGAATAAAATGTTTCTATTTTACAAAAAATAAAAAA

FIGURE 211

MENMFLQSSMLTCTIFLLISGSCELCAEENFSRSYPCEDEKKQNDSVIAECSNRRLQEVPTQTVG
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHONGNPGIQSNGLNITDGAFLNL
KNLRELLLEDNQLFPQIPSGLPESLTELSTLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV
CEKTNIEDGVFETLTNLLELLSLSFNSLSHVPPKLPSSLRKLFSLNTQIKYISEEDFKGLINL
TLDLDSGNCPRCFNAPFPCVPCDGGASINIDRFQNLTLQLRYLNLSSSTSLRKINAAWFKNM
PHLKVLDELFNYLVGEIVSGAFLTMLPRLEILDLSFNIIKGSYPQHINISRNFSKLLSLRAL
HLRGYVFQELREDDFQPLMQPLNLSTINLGINFIKQIDFKLFQNFNSNLEIIYLSENRISPLV
KDTROSYANSSSFQRHIRKRRSTDFEFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDELE
LDLSYNSHYFRIAGVTHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVPSGNRL
DILWDDDNRYISIFKGLKNLTRLDLNLRLKHIPNEAFLNLPASLTEHLHINDNMLKFFNWT
LLQQFPRLELLDLRGNKLLFLTDSLSDFTSSLRTLLLSHNRISHLPSGFLSEVSSSKHLDLS
SNLLKTINKSALETKTTTKLSMLELHGNPFECTCDIGDFRRWMDHEHLNVKIPRLVDVICASP
GDQRGKSIVSLELTTCVSDVTAVILFFFFFTFITTMVLAALAHHLFYWDVWFIYNVCLAKVK
GYRSLSTSQTIFYDAYISYDTKASVTDWVINELRYHLEESRDKNVLLCLEERDWDPLAIID
NLMQSIQSKKTVFVLTCKYAKSWNFKTAFYLALQRLMDENMDVIIFILLEPVLQHSQYLRL
RQRICKSSILQWPDNPKAEGLPWQTLRNVVLTENDSRYNMYVDSIKQY

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 826-848

FIGURE 212

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCTCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAGGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCTGAGGCCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGGCCACCATGGCCACGCTGGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA
GCAGCTCCTGCCCTGTCCGGGGGATGACTGATTCTCTCCGCCAGGCCACCCAGAGGAGAA
GGCCACCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT
CTGGTGTGTGGCAGTGGGCGGCACAGAGCACGCGCTACCGGCCCGGCCGTAGGGTGTGTGCTGT
CCGGGCTCACGGGACCTGTCTCCGAGTCGTTCTGTGCAGCGTGTGTACCAGCCCTTCCTCA
CCACCTGCGACGGGCACCGGGCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC
CGCAGCCCTGGGCTGGCCCTTGCAGGCCCTCGCTACGCGTGTGCCCCGGCTGGAAGAGGAC
CAGCGGGCTTCCTGGGGCTGTGGAGCAGCAATATGCCAGCCGCATGCCGGAACGGAGGGA
GCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA
GATGTGGATGAATGCAGTGTCTAGGAGGGGCGGCTGTCCCAGCGCTGCATCAACACCGCCGG
CAGTTACTGTGTCAGTGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC
CCAAGGGAGGGCCCCCAGGGTGGCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAA
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTGGC
CCCCTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGACCCCGGCAGCCTCC
TGGTGCACCTCTCCAGCAGCTCGGCCGTCATCGACTCCCTGAGCGAGCAGATTCTCTTCCTG
GAGGAGCAGCTGGGGTCTGTCTCTGCAAGAAAGACTCGTGAAGCTGCCCAGCGCCCCAGGCTG
GACTGAGCCCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCCCAACATGCTGGGGGTCCAG
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCTTCCTCTCTTCTCTCTCCCC
TTCCTCGGGAGGCTCCCCAGACCTTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC
CCCTGGCTACCCCCACCTTGGCTACCCCCAACGGCATCCCAAGGCCAGGTGGGCCCCCAGCTG
AGGGAAGGTACGAGCTCCCTGCTGGAGCTGGGACCCATGGCACAGGCCAGGCAGCCCCGGAG
GCTGGGTGGGGCTCAGTGGGGGCTGCTGCCCTGACCCCCAGCACATAAAAAATGAAACGTGA
AAAGGGCGGCCGCGACTCTAGAGT
CGACCTGCAGAAGCTTGGCCGCCATGGCCCACTGTTTATTGCAGCTTATAATGGTTACAAAT

09978188.101501

FIGURE 213

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAACQPPCRNGGSCVQPGRCR
CPAGWRGDTCCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTL CVPKGGPFRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

092818.10501
10501.8818260

FIGURE 214

GCCAGGCAGGTGGGCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCAAGCAAG
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC
AGCAGCATCAGAGCAGCCCCGTGGTTGGCAGCAAAGTTTCAGCTTGGCTGGGCCCGCTGTGA
GGGGCTTCGCGCTACGCGCTGCGGTCTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCTTAGC
AGTGGATGAGCAACCAACGGGGGCCCGGGAGGGGAAGTGGCCCCGAGGGAGAGGAACCCC
AAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG
CACAGGTGGCCCCACCACCCGGAGGAGCAGCTCCTGCCCTGTCCGGGGGATGACTGATTCTC
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGC
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCCTA
CCGGCCCGGCGTAGGGTGTGTGCTGTCCGGGCTCACGGGACCCCTGTCTCCGAGTCGTTCCG
TGCAGCGTGTGTACAGCCCTTCTCACCACCTGCGACGGGACCGGGCTGCGAGCCTTAC
CGAACCATCTATAGGACCGCCTACCGCCGAGCCCTGGGCTGGCCCTGCCAGGCCTCGCTA
CGCGTGTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCTGGGGCTGTGGAGCAGCAATAT
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCACTGCTAGGAGGGGCGGCTG
TCCCCAGCGCTGCATCAACACCGCCGCGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCC
TGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG
ACAGGAGTGGACAGTGCATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGTTGGACCTGCT
GGAGGAGAAGCTGCAGCTGGTGTGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC
ATGGGCTCCCGACCCCGCAGCCTCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGAC
TCCCTGAGCGAGCAGATTCTCTTCTGGAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGA
CTCTGTAAGTGTGCCCCAGCGCTCCAGGCTGGAAGTGGAGCCCTCACGCCGCCCTGCAGCCCCCATG
CCCCTGCCCAACATGCTGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC
AGGGCCTTCTCCTCTTCTCCTCCTCCCTTCTCGGGAGGCTCCCCAGACCTTGGCATGGGAT
GGGTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCTGGCTACCCCAACGGCA
TCCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC
CCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGGCTCAGTGGGGCTGCTGCCTGAC
CCCCAGCACATAAAAAATGAAACGTG

093788-101501

FIGURE 215

MRGSQEVLLMWLLVLA VGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTL CVPKGGP RVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

105701-3310/660

FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCACCACCCGAGGAGCAGTCTCTGC
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTTGGC
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGTGTGTCCGGGCTCAG
GGGACCTGTCTCCGAGTCGTTCTGTGCAGCGTGTGTACCAGCCCTTCTCACCACCTGCGAC
GGGACCGGGCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGACGCCCTGG
GCTGGCCCTTGCAGGCCTCGCTACGCGTGTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG
CCTGGCCGCTGCGCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA
ATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT
GCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCAAGGGAGGG
CCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGAATGAAGGAAGAAGTGCAGAG
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTGCTGGCCCCACTGCACA
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCTGGTGCACCTCC
TTCCAGCAGCTCGGCCGATCGACTCCCTGAGCGAGCAGATTTCCTTCTGGAGGAGCAGCT
GGGGTCTGCTCCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGGCTGGACTGAGCCCC
TCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTCCTCCTCCCCCTCCTCGGGAG
GCTCCCCAGACCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCTGGCTACC
CCCACCTGGGTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC
GAGTCTCCTGTGTGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGG
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAAATAAAAATGAAACGTG

0577881050

FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTL CVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

06/23/2014 10:51:41 AM

FIGURE 218

GGTTGCCACAGCTGGTTTAGGGGCCCGACCACTGGGGCCCTTGTGAGGAGGAGACGCTCCCGGCCCGGGAG
 GACAAGTCGTGCCACCTTTGGCTGCCGACGTGATTCCTCGGGACGGTCCGTTTCTGCTGCTCAGCTGCCGCGCG
 AGTTGGGTCTCCGTGTTTCAGGCGGGCTCCCTCTCTGCTCTCCCTCTCCGCTGGGCGGTTTATCGGGAGG
 AGATTGTCTTCAGGGCTAGCAATTGGACTTTGATGATGTTTGACCCAGCGGACAGGAATAGCAGGCAACGTGAT
 TTCAAAGCTGGGCTCAGCCTCTGTTTCTCTCTCGTGAATCGCAAAACCCATTTTGGAGCAGGAATTCCAATCA
 TGTCTGTGATGTTGGTGAGAAAGGAGTGACACGGAAATGGGAGAACTCCAGGACAGGAACACCTTTTGTCTGTG
 ATGGCCCGCTCATGATGGCCCGGCAAAAGGGCAATTTCTAAGTACCTTTTCTCATCTCTGGGACATGTACAC
 TCTTCTTCGCTTGTAGTGCCCTACCTGGCTGTTGAGTGTCTCTGCCATCCCTGTATTTGCTGCCATGCTCT
 TCCTTTTCTCCATGGCTACACTGTTTGGAGACAGCTTCAGTGACCTGGAGTGATTCTCTGGGCGCTACCAAGTG
 AAGCAGCTTTCATAGAAATGGAGTAGAAGCTACCAATGGTGCGGTGCCCGAGGAGGAGCGACCAACGCTCGTA
 TCAGAAATTTCCAGATAAACCAACAGATTTGAAACTGAAATACGTTCACATGCAAGATCTTCGGGCTCCCG
 GGGCTCCCATGTCAGCATCTGTGACAACTGTGTGGAGCGCTTGACCATCACTGCCCTGGGTGGGAAATTTGTG
 TTGAAAGAGGAACTACCGCTACTTTACCTCTTCATCTTTCTCTCTCCCTCCCAATCTATGTCTTCGCT
 TCAACATCGTCTATGTGGCCCTCAAACTTTGAAATTTGGCTTCTTGGAGACATTTGAAAGAACTCTTGGAACTG
 TTCTAGAAGTCTCATTTGCTTCTTTACACTCTGGTCCGTGGGAGTGAATGGATTTCACTCTTCTCTGCTG
 CTCTCAACAGACCAACCAATGAAGACATCAAGGATCATGGACAGGAGAAATCGCTCCAGAACTCCCTACAGCC
 ATGGCAATTTGTGAAGAACCTGTGAACTGCTGTGGCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGTA
 TTTTGCACTGGAGGAAAGTGAAGTGCAGCTCCCACTCTCAAGAGACAGTACAGCTCTTGCACAGAGCC
 CAGGCCACAGAACCAACTGAATGAGATGCCGAGGACAGCAGCACTCCCAAGAGATGCCACTCCAG
 AGCCCCACAGCCACAGGAGGAGCTGAAGCTGAGAAGTAGCCTATCTATGAAGAGACTTTTGTTTGTGTT
 TAAATTAGGCTATGAGAGTTTCAGGTGAGAAGTAAACTGAGACAGAGCAGTAAGCTGTCTCTTTTAACT
 GTTTTCTTCTGCTCTTTAGTCAACCAGTTGCACACTGGCAATTTCTGCTGCAAGCTTTTTTAAATTTCTGAAC
 CAAGCACTGGCAGAGATGTGAGTCACTCTGATAACTGGAAAAATGGGTCTCTTGGGCCCTGGCACTGGTTCT
 CCATGGCTCAGCACAGGGTCCCTTGGACCCCTCTCTTCCCTCAGATCCCGGCCCTCTGCTTGGGGTCA
 TGGTCTCATTTCTGGGGCTAAAGTTTGTGAGACTGGCTCAAACTCTCCCAAGCTGTGCACTGTCTGAGTCCAGA
 GGCAGTCAAGAGACTCTGCGCAGGGGATCTAAGTGGGTCTTGGGGTCTTGGAGTGAAGAGGAGGAGAG
 TGGGTGAGAAATTTCTCTGCCACCAAGTCCAGCATTTGCCCAAACTCTTTAGGAATGGGACAGGTACCT
 TCCACTTGTGTANNNNNNNNNNNNNNNNNNNNNNNNNNNNNTGTTTTTCTCTTTGACTCTGCTCCATTAGGAG
 CAGGAATGGCAGTAATAAAGTCTGCACCTTTGCTCATTTCTTTCTCTCAGAGGAGCCCGAGTGTCTCACTTAAAC
 ACTATCCCTCAGACTCCCTGTGTGAGGCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG
 GCTCTCTCTCTCTCTCTCTCTCCCCGATGTAACCTCAAAAAAATAAATGCTTAACAGTTTCTCCATTAAGCT
 CGGCTGAGTGAAGGAAAGCCAGCACTGCTGCCCTCTCGGGTAACTCAACCTAAGGCTCGGCCACCTCTGGCT
 ATGTGTAACCACTGGGGGCTTCTTCAAGCCCGCTCTTCCAGCACTTCCACCGGAGAGTCCAGAGCCACTT
 CACCTGGGGTGGGCTGTGGCCCGAGTCAGCTCTGCTCAGGACCTGCTCTATTTAGGGAAGAGATTATATG
 ATTATGTGTGGCTATATTTCTAGAGCACTGTGTTTCTCTCTTCTAAGCCAGGGTCTGTCTGGATGACTTAT
 GCGGTGGGGGATGTAAACCGGAATTTTCACTATTTTGAAGGCGATTAAACTGTGCTATGTCGA

0978188-101501

FIGURE 219

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGFYLTFLILGTCTLFFAFECRYLAV
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNVERFDHHCPWVGNCV GKRNRYFYFL
FILSLSLTLTYVFAFNIVYVALKSLKIGFLET LKETPGTVLEVLCFPTLWSVVGLTGPHTF
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVL CGPLPPSVLDRRGILPLEESGSR
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPEPPEPPQEAAEA EK

Putative transmembrane domains:

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

FIGURE 220

AAAACCCTGTATTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT
CCCACAGAGCNCCTTCGACCATCACTGCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTA
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA
ACATCGT

105107.8878262

FIGURE 221

GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGCACAAAAAGAAGAAAAAGAAGA
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGGCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCTCAGGTGCACTATT
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
CAAGTGGTGCTCGATCCTCGCGTGGTCTCTCTGAGCAACCCAAACGAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATGTAGAGATTTT
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACATATCCACCATA
TTTCAGAAGCCCAAGGTACAGGTGTCCCGTGGGACAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCTCTCAAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAACTACACTTGGCTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTATTGGTCCAGGCGCCGTGAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCTCTTCTGCTTGTGACCTGCTTCTCAAAATTTTGATGTGAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAGAGTTTTAAAAAAGAAATTGAA
AATTGCCTTGACAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAACCGGAAGAACAACAGC
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCACCTCTTTGGTGGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA
AAAAA

007733-1054

FIGURE 222

MKTIQPKMHNSISWAIPTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVVDVYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL
EIQGITREQSGDYECASNDVAAPVVRVKVTNYPPISEAKGTGVFVGQKGTLCQCEASAV
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNKLGHTNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLKLF

Signal peptide:

amino acids 1-28

105101.88182660

FIGURE 223

GAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT
GACAAGTGGTGCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA
ACCACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAATTTGTAGAGATT
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG
ACCAGAG

0978188:10501

FIGURE 224

ATGGCTGGTGACGGCGGGGCCGGGACCGGGGCCGCGGCCGGGAGCGGGCCAGCTGCCGGAGCCCTGA
 ATCACCCCTTGGCCCGACTCCACATGAACGTTGCGCTGCGAGCTGCGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG
 AAGGGGACAGACAGCTGTGTAGGCTCACGACCGCAGCTGGAGCTGCTTTAGCAGGTGCCCTCTACTGCTGGCT
 GCAGTGCTTCTGGGCTGCTTGTGCGCTTAGGGTCCAGTACCACAGAGACCATCCACAGCACCTTGCTTACA
 GAGGCTTCGATTCGAGTGGCTGGAAAAATCTGGAGTCCCTTGGAACCGAGGGGTGAGCCCTGTGAGGACTTTTAC
 CAGTTCTCTGTGGGGCTGGATTCTGGAGAACCCCTTGCCGATGGGGCTTCTGCTGGAACACCTTCAACAGC
 CTCTGGGACCAAAACAGGCCATCTGAAGCACTGCTGTGAAAAACACCACTTCAACTCCAGCAGTGAAGCTGAG
 CAGAAGACACACGCTTCTACCTATCTTGCTTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCAGCCACTGAGA
 GACCTCATTTGAGAAGATTGGTGGTTTGGAACTTACGGGGCCCTGGGACAGGACAACTTTATGGAGGTGTTGAAG
 GCAGTAGCAGGACCTACAGGGCCACCOCATTTCTACCGTCTCATCATGTCGCGACTCTAAGAGTTCCAAACAGC
 AATGTTATCCAGGTGGACAGTCTGGCTCTTTCTGCGCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG
 AAAGTGCTCAGTGCCTATCTGGATTACATGGAGGAACTGGGGATGCTGCTGGGTGGGCGGCCACCTCCACAGGAG
 GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAAATCAACAGTGCCCCAGGACCAAGCGCGCGAC
 GAGGAGAAGATCTACCAAGATGAGCATTTGCGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTT
 CTGCTTTCTTGTGTCAACATTGGAGTTGAGTGACTCTGAGCCTTGGTGGTGTATGGGATGGATTATTTGCGAG
 CAGGTGTTCAGAGCTCATCAACCGCACGGAACCAAGCATCTGAAACAATTACCTGATCTGGAACCTGGTGCAAAAG
 ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCTCTATGGGACTAAGAAG
 TCCTGTGTGCGAGGTGGCAGCCTGCATCTCCAACACGGATGACGCGCTTGGCTTGTCTTGGGGTCACTCTTC
 GTGAAGGCCACGTTTTCGCGGCAAGCAAGAAATTGACAGGGGATGATCAGCGAAATCCGGAACCGCATTTGAG
 GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCGCCAGGACAGCAAGGAGAAACAGATGCCATCTAT
 GATATGATTGGTTTCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGATGTTTATGAACGGGTACGAAATTTC
 GAAGATTCTTTCTCCAAACATGTTGAATTTGTACAATCTCTGCGCAAGGTTATGCTGACCAAGCTCCGCAAG
 CCTCCAGCCGAGACCAAGTGGAGCATGACCCCCAGACAGTGAATGCTACTACTTCCAACCTAAGAATGAGATC
 GTCTTCCCGCTGGCATCTGCGAGGCCCTTCTATGCGCGCAACCAACCCCAAGGCCCTGAACTTCTGGTGGCATC
 GGTGTGGTCAATGGCCATGAGTTGACGCATGCTTTGATGACCAAGGGCGCGATATGACAAAGAGGGAACCTG
 CGGCCCTGGTGGCAGATGAGTCCCTGGCAGCTTTCGGAACCAACCGGCTGCATGGAGGAACAGTACAATCAA
 TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCAAGACGCTGGGGAGAACATTACTGACAAACGGGGGCTGAAG
 GCTGCGTACAATGCTTACAAGCATGGCTGAGAAAGCATGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC
 AACCACCAAGCTCTTCTTCTGGTGGATTGCCCCAGTGTGCTGCTGGTCCGACACACAGAGAGCTCTCAGAGGGG
 CTGGTGACCGACCCCAACAGCCCTGCCCCGCTTCCGCTGCTGGGCACTCTCTCAACTCCCGTGACTTCTCGGG
 CACTTGGCTGCCCTGTGCGCTCCCCATGAACCCAGGCGAGCTGTGAGGTTGGTGAACCTGGATCAGGGGA
 GAAATGGCCAGCTGTCAACAGCACTGGGGCAGCTCTCTGACAAAGCTGTGTTCTTGGGTTGGGAGGAAGCAA
 ATGCAAGCTGGGCTGGCTTACTGCTTCCCCCCACAGGTGACATGAGTACAGACCTCTCAATCACCACATTG
 TGCTCTGCTTGGGGTGGCTTCCCTGCTCCAGCAGAGCCCCACCACTTCACTGTGACATCTTTCGCTGTACCC
 GCCTGGAAGAGGTCTGGTGGGGAGGCCAGTTCCATAGGAAGAGTCTGCC

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FIGURE 225

MNVALQELGAGSNVGFQKGTQQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSH
STCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLDGRSRWNTFNSLWDQNQA
ILKHLLENTTFNSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGWNITGPWDQDN
FMEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGFLPLPSRDYYLNRTANEKVLTA
LDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP
SMDWLEFLSFLLSPLELSDSEPVVVGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL
DRRFESAQEKLETLTYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKETAEGLMI
SEIRTAEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVVDGYEISEDSF
PQNMLNLNYPFAKVMADQLRKPPSRDQWSMTPQTVNAYYLPKNEIVFPAGILQAPFYARNH
PKALNFGGIGVVMGHELTAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQV
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCS
VRTPESSHEGLVTDPHSPARFVLGTLSNSRDFLRHFGCPVGSPMNPGLCEVW

Type II Transmembrane domain:

amino acids 32-57

Introduction

[illegible]

FIGURE 227

GGCCGAGCGGGGGTGTGCGCGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA
CCGGGGCCCGCGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCTGGCCCCGAC
TCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA
TCCCACAGCACCTGCGCTTACAGAGGCCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCT
GGACCGAGGGGTGAGCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTTCGGA
GGAACCCCTGCCCAGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA
GAAGACACAGCGCTTCTACCTATCTTGCCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCATTCTTCAC
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC
ATCTTCCGAACCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT
TTGCCAAGGCTCAGAGCAGGAAGGTGAGCCTATCCTGTACCTAGTGAACAACTGCCCT
CCTTTCTTTCTTCTTTTCTCCTCCCTCCCTCCCTTCTTCCCCTTTTCTTCTTCTTCTTCC
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTCG
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTGATGGGTTCATGGACCT
AGATAGGCTGATAACAAAGCTCACAAAGAGGGTCTTCTGAGGATTACGAGAGACTTATGGAGCC
AGCAAAGTCTTCTGAAGAGATTGCATTGAGCCAGGTCTGTAG

FIGURE 228

ATGCCTACTACCTTCCAAC TAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC
TTCTATGCCCCGCAACCACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAG
TACAATCAATAC CAGGTCAATGGGGAGAGGCTCAACGCCCGCCAGACGCTGGGGGAGAACAT
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCAC CAGCTCTCTTCGTGGGATTT
GCCCAGGTGTGGTGTCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGCTGGTGACCGACCC
CCACAGCCCTGCCCCTTCCGCGTGTGGGCACTCTCTCAACTCCC GTGACTTCTTGCGGC
ACTTCGGCTGCCCTGTGCGCTCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC
TGGA TCAGGGGAGAAATGGCCAGCTGTCAACGAGCCTGGGGCAGCTCTCCTGACAAAGCTGT
TTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCCA
GGTGACATGAGTACAGACCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCT
GCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGTGTACCCCTGCCTGGAAGAG
GTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCCTCTTCTGTCCCAGGCTCACT
CAGCCTGGCGCCATGGGGCTGCCGTGCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG
TACCTCCTGGACTTCTCCCAGGCTCACTCAGTGC GCACTTAGGGGTGGACTCAGCTCTGTC
TGGCTCACCTTCACGGGCTACCCCCACCTCACCTGTGCTCCTTGTGCCACTGCTCC CAGTG
CTGCTGTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCTCTGAAAGCCTCCTGC
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTG CATATGTGTAGCGGTACTGGTTCCTGT
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAGCAGGAAAGCAGATA
GAGCAGGGAAGGAAGAACAGAGTTTATTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT
TGGCCCTTATAGGACC

0397338.101501

FIGURE 229

CCCACGCGTCCGAGCCGCCCGAGAATTAGACACACTCCGGACGCGGCCAAAAGCAACCGAGA
 GGAGGGGAGGCAAAAACACCGAAAAACAAAAAGAGAGAAACAACCCCAACAACCTGGGGTGG
 GGGGAAGAAGAAAGAAAAAGAAACCCACCCACCCAAAAAAGAAAAAAGAAAAA
 AAAAAAAGAAATCCTGTGGCGCGCCGCTGGTCCCGGGAAGACTCGCCAGCACCAGGGGG
 TGGGGAGTGGAGCTGAAAGCTGCTGGAGGTGAGCAGCCCTAGCAGGGATGGACATGATG
 CTGTTGGTGCAGGGTCTTGTGTCTCGAACAGTGGCTGGCGGGTGGCTCTCAGCCCTGTG
 CTGCTGTCTACCTCTCGCTCCCGGCTGGACAGAGTGTGGACTTCCCTCGGCGGCGCTGG
 ACAACATGATGGT CAGAAAGGGGACACGGCGGTGCTTAGGTGTTTATTTGGAAGATGGAGCT
 TCAAAGGGTGGCTGGCTGAACCGGTCAAGTATTATTTTTCGGGAGGTGATAAGTGGT CAGT
 GGATCCTCGAGTTTCAATTTCAACATTGAATAAAGGGACTACAGCCTCCAGATACAGAATG
 TAGATGTGACAGATGATGGCCCATACAGTGTCTGTTCAGACTCAACATACACCAGAACA
 ATGCAGGTGCATCTAACTGTGCAAGTTCCTCCTAAGATATATGACATCTCAAATGATATGAC
 CGTCAATGAAGGAACCAACGTCACTCTTACTTGTGGCCACTGGGAAACAGAGCCTTCCA
 TTTCTTGGCGACACATCTCCCCATCAGCAAAACCATTTGAAATGGACAATATTTTGGACATT
 TATGGAATTACAAAGGACAGGCTGGGGAATATGAATGCAGTGGCGGAAATGCTGTGT CATT
 CCCAGTGTGAGGAATGAAAGTTGTGTCAACTTTGCTCCTACTATTCCAGGAATTAAT
 CTGGCACCGTGACCCCGGACGCAGTGGCCTGATAAGATGTGAAGGTGCAGGTGTGCCGCT
 CCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCTCTTCAATGGCCAAACAGGAATTTATTAT
 TCAAAATTTAGCACAGATCCATTCTCACTGTTACCAACGTGACACAGGAGCACTCGGCA
 ATTATACCTGTGTGGCTGCCAACAAAGCTAGGCACAAACCAATGGCAGCCTGCTCTTAACCT
 CCAAGTACAGCCCGAGTGAATTAACGGGAGCGTGATGTTCTTTCTCCTGCTGGTACCT
 TGTGTTGACACTGTCTCTTTTACCAGCATATTTCTACCTGAAGAATGCCATTCTCAAAATA
 TTCAAAGACCCATAAAGGCTTTTAAGGATTTCTCTGAAAGTGTGATGGCTGGATCCAATCT
 GGTACAGTTTGTAAAGCAGCGTGGGATATAATCAGCAGTGCTTACATGGGGATGATCGCC
 TTTCTGTAGAATTGCTCATTATGTAAATACTTTAATTTCTACTCTTTTTTGATTAGCTACATTA
 CTTTGTGAAGCAGTACACATTGTCTTTTTTAAAGACGTGAAGGCTCTGAAATTTACTTTTAG
 AGGATATTAATTTGATTTTCATGTTTGTAAATCTCAAACTTTTCAAAGCATTCACTCATGGT
 CTGCTAGGTTGCAGGCTGTAGTTTACAAAAACGAATATTGCAGTGAATATGTGATTCTTTAA
 GGCTGCAATACAAGCATTCACTCCCTGTTTCAATAAGAGTCAATCCACATTTACAAAGATG
 CATTTTTTTTCTTTTTTGATAAAAAAGCAAATAATTGCGCTCAGATTATTTCTTCAAAATA
 TAACACATATCTAGATTTTTCTGCTTGCAATGATATTCAGGTTTCAGGAATGAGCCTTGTAA
 ATAACTGGCTGTGCAGCTGCTTCTCTTTCTGTAAGTTCAAGATGGGTGTGCTTTCATAC
 AATAATATTTTTCTCTTTGCTCCAACATAATAAATGTTTTGCTAAATCTTACAATTTGA
 AAGTAAAAATAACAGAGTGAATCAAGTTAAACCATACACTATCTCAAGTAAACGAGGAGC
 TATTGGACTGTAAAAATCTCTTCTGCACGTACAATGGGGTTTGAGAATTTTGCCCCACACT
 AACTCAGTTCTTGTGATGAGAGACAAATTAATAACAGTATAGTAATATACCATATGATTTT
 TTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGAAATCACTCCCTTTAAATGACAGCACA
 GTCCACTCAAAGGATTGCCTAGCAATACAGCATTTTTCTTTCTACTAGTCCAAAGCCAAAAA
 TTTTAAGATGATTTGTGAGAAAGGGCACAAAGTCTATCACCTAATATTACAAGAGTTGGTA
 AGCGCTCATCATTAATTTTATTTTGTGGCAGGTATTAGACAGTCAAGCTGGAGGCTATGCG
 TATGGATATGGACGTTCCAGAGACTATAATGGCAGAAACGAGGTGGTTATGACCGCTACTC
 AGGAGGAATTAACAGACAAATATGACAACTGAAATGAGACATGCACATAATATAGATACA
 CAAGGAATAATTTCTGATCCAGGATCGTCTTCCAAATGGCTGTATTTTAAAGGTTTTTGG
 AGCTGCACCTGAAGCATTTTATTTATAGTATATCAACCTTTTGTTTTTTAAATGACCTGCCA
 AGGTAGCTGAAGACCTTTTATAGACAGTTCATCTTTTTTTTTTAAATTTTCTGCTCATTTTAA
 AGACAAATTTATGGGACGTTTGTCAAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 230

MMLLVQGACCSNQWLAAVLLSLCCLLPSCLPAGQSVDFPWAAVDNMMVRKGD TAVLR CYLED
GASKGAWLNRSSII FAGGDKWSVDPRVSI STL NKR DYS LQIQ NV DVTDDG P YTC SVQT QHTP
RTMQVHLTVQVPPKIYDISNDMTVNEGTNVTLTCLATGKPEPSISWRHISPSAKPFENGQYL
DIYGITRDQAGEYEC SAENAVSFPDVRKVKVVVNFAPT IQEIKSGTVTPGRSGLIRCEGAGV
PPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVINVTQEHFGNYTCVAANKLGT TNASLPL
NPPSTAQYGITGSADVLFSCWYLVLTLSSFTSIFYLKNAILQ

Important features of the protein:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 326-345

N-glycosylation sites.

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

Casein kinase II phosphorylation site.

amino acids 147-151, 208-212, 224-228

Tyrosine kinase phosphorylation site.

amino acids 178-186

N-myristoylation sites.

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,
302-308, 319-325

Myelin P0 protein:

amino acids 92-121

FIGURE 231

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTCTTGCTGG
CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGA
CGAGCTCTTGAGTGAGACCCACAAGCTGCTTTTACCACAAATTGCAATGGAGCCTTTTGGAAA
TCAATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACTTCTCCCTAGCTGTGGTGGTCATC
TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC
GCGGCTCCGGTCTTGGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT
CCTTCTCCTTGCTGCAGTCAGCACACCTGGAGAACCTGGCTCAGGGTGCATCGAGGCTG
CAAGTCCTGCAGGCCAACTCACCTGGGTCGCGCTCAGCCATGAGCACTTGCTGCAGCGGT
AGACAACTTCACTCAGAACCCAGGGATGTTTCAAGTCAAGGTGAACAAGGCGCCCAAGTC
TTCAAGGTCAACAAGGGGCCATGGGCATGCTGGTGCCTTGGCCCGCGGGACCACTGCT
GAGAAGGGAGCCAAGGGGCTATGGGACGAGATGGAGCAACAGGCCCCCTCGGGACCCCAAGG
CCCAACGGGAGTCAAGGGAGAGGCGGGCTTCCAAGGACCCAGGGTGTCTCAGGGAAGCAAG
GAGCCACTGGCACCCAGGACCCCAAGGAGAGAAGGGCAGCAAGGCGATGGGGGTCTCATT
GGCCCCAAAAGGGGAACTGGAACTAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA
AGGGGACAGGGGCATGAAAGGAGATGCAGGGGTGCTGGGGCTCTTGGAGCCAGGGGAGTA
AAGGTGACTTCGGGAGGCCAGGCCACCAGGTTTGGCTGGTTTTCTTGGAGCTAAAGGAGAT
CAAGGACAACCTGGACTGCAGGGTGTTCGGGGCTCTTGGTGCAGTGGGACACCCAGGTGC
CAAGGGTGAGCCTGGCAGTGTCTGGCTCCCTTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGA
GTCCAGGAGCCACAGGCCTGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGA
AGAAAAGGAGAATCAGGAGTTCAGGCCCCTGACAGGTGTGAAGGGAGAACAGGGGAGCCAGG
GCTGGCAGGTCCCAAGGGAGCCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAGGTGAAAGAGGTGAAAACCTCAGTGTCC
GTCAGGATTGTTCGGCAGTAGTAACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGG
GACAATTTGCGATGACGAGTGGCAAAATTTCTGATGCCATTGTCTTCTGCGCATGCTGGGTT
ACTCCAAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT
GTTCACTGTTCGGGGCACGGAGAGTACCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCA
TGACTGCAGCCACGAGGAGGACGCGAGGCTGGAGTGCAGCGTCTGACCCCGGAAACCCCTTCA
CTTCTCTGCTCCCGAGGTGTCTCTGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT
TCCCTGGGGACAACCTGAGCAGCCTCTGGAGAGGGGCCATTAATAAAGCTCAACATCATTGA

FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAFAHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL
LVVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLQSAHPGEHLAQGASRLQVLQALTWVR
VSHHLLQRVDNFTQNPGMFRIKGEQQAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRD
GATGPSGPQGPVKEAGLQGPQGA PGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGE
KGDGLPGSKGDRGMKGDAGVMGPPGAQGSKGDGFRPGPPGLAGFPKAGKDGQGPGLQGVPG
PPGAVGHHPGAKGEPGSAGSPGRAGLPGSPGSGATGLKGSKGD TGLQGGQGRKGESGVPGPA
GVKGEQGSFPLAGPKAPGQAGQKGDQGVKGSSGEGQGVKEKGERGENSVSVRIVGSSNRGR
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLNDNVQCRGTESTLW
SCTKNSWGHHDCSHEEDAGVECSV

Transmembrane domain:

amino acids 47-66 (type II)

N-glycosylation sites.

amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.

amino acids 432-440

N-myristoylation sites.

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521

Amidation site.

amino acids 360-364

Leucine zipper pattern.

amino acids 56-78

Speract receptor repeat

amino acids 422-471, 488-519

Clq domain proteins.

amino acids 151-184, 301-334, 316-349

FIGURE 233

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTTGTAAGAAGCTCCTTCCAGCACCTCCTCT
CTTCTCCTTTTGCCCAAACCTACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG
ACCAAAAGGAAAGAAGAAAAAGGGCCAAAAGCCAAAATGAACTGATGGTACTTGTTTTCAC
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA
GAAAGATACTAAAAGATCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG
CAACTTCAGCGAATTGCTCTGCTGCCCAAAGACGTTTTCTTTGGACCAAGATCTCTTTCG
TGATTCTTGCAACAATCAATTGAGAATCTTCATGTATTCTGGAGAACACCATTCTGTATTC
CCACAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT
AGATTCTATAAATTCTTACTTGCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA
AGTTAATTCAATCTAAAAAAAAAAAAA

FIGURE 234

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758
<subunit 1 of 1, 98 aa, 1 stop
<MW: 11081, pI: 6.68, NX(S/T): 1
MKLMVLVFTIGLTLLLGVPANRLSCYRKILKDHNCNLPQGVADLTQIDVNVQDHFWDG
KGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-76

Tyrosine kinase phosphorylation site.

amino acids 63-71

FIGURE 235

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGCTCGGAGCGAATTCAGCCTGCAGGG
 CTGATAAGCGAGGCATTAGTGAAGATTGAGAGAGACTTTACCCCGCGTGGTGGTTGGAGGGC
 GCGCAGTAGAGCAGCAGCACAGCGCGGGTCCCGGAGGCCGGCTCTGCTCGCGCCGAGATG
 TGGAAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACCGCGCGCCGCCGCTGGCTGTG
 CGCTGGGGCGCTGGTGTGCGGGTGGCTTCTTCTCCTCGGCTTCCTCTTCGGGTGGTTTA
 TAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAGCATTTTGGAT
 GAATTGAAAGCTGAGAACATCAAGAAGTCTTACATAATTTTACACAGATACCACATTTAGC
 AGGAACAGAAACAAATTTTCAGCTTGCAGAACCAATTCAAATCCCAAGTGAAGAAATTTGGCC
 TGGATTCTGTTAGCTAGCTCATTATGATGTCCTGTTGCTTACCCAAATAAGACTCATCCC
 AACTACATCTCAATAATTAATGAAGATGGAATGAGATTTTCAACATCATTTATTGAACC
 ACCTCCTCCAGGATATGAAAAATGTTTCGGATATGTACCCACCTTTTCAGTGCTTCTCTCCTC
 AAGGAATGCCAGAGGGCGATCTAGTGTATGTTAACTATGCACGAACTGAAGACTTCTTTAA
 TTGGAACGGGACATGAAATCAATTGCTCTGGGAAATTTGTAATTGCCAGATATGGGAAAGT
 TTTTCAGAGGAAATAAGGTTAAAAATGCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACT
 CCGACCTGCTGACTACTTTGCTCCTGGGGTGAAGTCTATCCAGACCGGTTGGAATCTTCTCT
 GGAGGTGGTGTCCAGCGTGGAAATATCTAAATCTGAATGGTGCAGGAGCCCTCTCACACC
 AGGTTACCCAGCAATGAATATGCTTATAGCGCTGGAATTGCAGAGGCTGTTGGCTCTCCAA
 GTATTCCTGTTTCATCCAATTGGATACTATGATGCACAGAAGCTCTAGAAAAAATGGGTGGC
 TCAGCACCCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG
 CTTTACTGGAACCTTTTCTACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA
 CGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGAACCAGACAGATATGTCATT
 CTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCTCAGAGTGGAGCAGCTGT
 TGTTTCATGAAATTTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACTTAGAAGAA
 CAATTTGTTTGCAGAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTAGTGTGGCA
 GAGGAGAATTCAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTAT
 AGAAGGAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTCGGTACACAACC
 TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAACTCTTTTATGAAAGTTGG
 ACTAAAAAAGTCCCTCCCCAGAGTTTCAGTGGCATGCCAGGATAGCAAAATTTGGGATCTGG
 AAATGATTTTGGGTGTTCTTCCAACGACTTGAATTTGCTTCAGGCAGAGCACGGTATACTA
 AAAATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCAAGTGTCTATGAAACATAT
 GAGTTGGTGGAAAAGTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCAGGTTTCG
 AGGAGGGATGGTGGTTGAGCTAGCCAATTCATAGTGCTCCCTTTGATTGTGCGAGATTATG
 CTGTAGTTTAAAGAAATGATGCTGACAAATCTACAGTATTTCTATGAAACATCCACAGGAA
 ATGAAGACATACAGTGTATCATTTGATTCACTTTTTTCTGCAGTAAAGAATTTTACAGAAAT
 TGCTTCCAAGTTTCAGTGGAGAGACTCCAGGACTTTGACAAAAGCAACCCAATAGTATTAAGAA
 TGATGAATGATCAACTCATGTTTCTGGAAGAGCATTTATTGATCCATTAGGGTTTACCAGAC
 AGGCCCTTTTATAGGCAATGTCATGTCTCAAGCAGCCACAAGATATGCAGGGGAGTCT
 ATTCACAGGAATTTATGATGCTCTGTTTGTATATTGAAAGCAAAGTGGGACCTTCCAGGCCCT
 GGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCTTCAGAGTCAGGCAGCTGCAGAGACT
 TTGAGTGAAGTAGCCTAAGAGGATTTTATGAGAATCCGATATTGAAATTTGTTGGTATGTCAC
 CTCAGAAAGAATCGTAAATGGGTATATTGATAAATTTAAAAATGGTATATTGAAATAAAGT
 TGAATATTATATATAA

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756
><subunit 1 of 1, 750 aa, 1 stop
><MW: 84305, pI: 6.93, NX(S/T): 10
MWNLHETDSAVATARRPWLACAGALVLAGGFLLGFLFGWFIKSSNEATNITPKHNMKAFL
DELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTH
PNYISIIINEDGNEIFNTSLFEPPPPGYENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFF
KLERDMKINCSCGKIVIRYGVFRGNKVNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNL
PGGGVQQRGNILNLNAGDPLTPGYPANERYARRGIAEAVGLPSIPVHPIGYYDAQKLEKMG
GSAPPDSSWRGSLKVPYNVPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDYRV
ILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEW
AEENSRLLQERGVAIYNADSSIEGNYTLRVDCITPLMYSLVHNLTKELKSPDEGFEGKSLYES
WTKKSPSPPEFSGMPRIKSLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLVHSVYET
VELVEKFYDPMFKYHLTVAVQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYSISMKHPQ
EMKTYSVSFDLSFAVNKFTETIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLP
DRPFYRHVIYAPSSHNNKYAGESFPFIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAE
TLSEVA

Signal sequence:

amino acids 1-40

N-glycosylation sites.

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,
459-463, 476-480, 638-642

Tyrosine kinase phosphorylation sites.

amino acids 363-372, 605-613, 606-613, 617-626

N-myristoylation sites.

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,
360-366, 427-433, 529-535, 707-713